

79576

From: Chan, Christina  
 Sent: Wednesday, November 06, 2002 1:16 PM  
 To: Holleran, Anne; STIC-Biotech/ChemLib  
 Subject: RE: RUSH search for 09/480,977

## Please rush. Thanks Chris

Chris Chan  
 TC 1600 New Hire Training Coordinator and SPE 1644  
 308-3973  
 CM-1, 9B19

-----Original Message-----

From: Holleran, Anne  
 Sent: Wednesday, November 06, 2002 9:52 AM  
 To: Chan, Christina  
 Subject: RUSH search for 09/480,977

Point of Contact:  
 Mona Smith  
 Technical Information Specialist  
 CM1 6A01  
 Tel: 308-3278

Please approve and forward to STIC the following sequence search request. This case is an amendment due this biweek. Thanks.

Please search the following:

commercial and interference database search of SEQ ID NO: 4(aa)

Anne Holleran  
 AU: 1642  
 Tel: 308-8892  
 RM: 8e03

mailbox: 8e12

Searcher: H. Smith  
 Phone: \_\_\_\_\_  
 Location: \_\_\_\_\_  
 Date Picked Up: 11/7/02  
 Date Completed: 11/8/02  
 Searcher Prep/Review: 5  
 Clerical: \_\_\_\_\_  
 Online time: 5

TYPE OF SEARCH:  
 NA Sequences: \_\_\_\_\_  
 AA Sequences: 1  
 Structures: \_\_\_\_\_  
 Bibliographic: \_\_\_\_\_  
 Litigation: \_\_\_\_\_  
 Full text: \_\_\_\_\_  
 Patent Family: \_\_\_\_\_  
 Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
 STN: \_\_\_\_\_  
 DIALOG: \_\_\_\_\_  
 Questel/Orbit: \_\_\_\_\_  
 DRLink: \_\_\_\_\_  
 Lexis/Nexis: \_\_\_\_\_  
 Sequence Sys.: \_\_\_\_\_  
 WWW/Internet: \_\_\_\_\_  
 Other (specify): \_\_\_\_\_

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen, Ltd.

On protein - protein search, using sw model

Run on: November 7, 2002, 09:59:10 ; Search time 26 seconds

Scoring table: BLASUM62 312.722 Million cell updates/sec

Title: US-09-480-977-4

Perfect score: 277

Sequence: 1 HEKPCRDQLAYCLNIDGCEC... SHKHICRCKBQYQGVRCDFEL 47

Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL.19:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rabbit:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacterioplasm:\*
- 17: sp\_archeab:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match Length	DB	ID	Description	PRELIMINARY	PRT;	461 AA.
1	113.5	41.0	461	11	035947	ID 035947; PRELIMINARY; PRT; 461 AA.			
2	111.5	40.3	298	11	09ESA9	AC 035947; DT 01-JAN-1998 (TREMBREL. 05, Created)			
3	111.5	40.3	695	11	09ESB0	DT 01-JAN-1998 (TREMBREL. 05, Last sequence update)			
4	104.4	37.7	241	6	007112	DT 01-JUN-2001 (TREMBREL. 17, Last annotation update)			
5	104.5	37.7	296	4	0961B3	DE PRO-NEUREGULIN-1, ISOFORM ALPHA 2B PRECURSOR, NRG1 OR NDF.			
6	102.5	37.0	111	11	09ESA8	OS Mesocricetus auratus (Golden hamster).			
7	102.5	37.0	136	11	09ESA7	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.			
8	102.5	37.0	256	11	09ESA6	OX NCBI_TaxID=10036;			
9	102.5	37.0	317	11	09ESA3	[1] SEQUENCE FROM N.A. (ISOFORM ALPHA2B), AND SEQUENCE OF 64-81.			
10	102.5	37.0	323	11	09ESA2	RC TISSUE=EMBRYO;			
11	102.5	37.0	342	11	09ESA1	RA MEDLINE=98195996; PubMed=9557646; Velasco J.A., Feijoo E., Avila M.A., Notario V.;			
12	102.5	37.0	700	11	09ESB1	RT "Secretion of neu differentiation factor-like polypeptides by coph-transformed fibroblasts: cloning and characterization of syrian hamster neurogulin cDNAs.";			
13	102.5	37.0	782	11	09ESA5	RT Mol. Carcinog. 21:156-163 (1998).			
14	99.9	35.7	89	12	09IM20	CC -1- FUNCTION: DIRECT LIGAND FOR ERBB3 AND ERBB4 TYROSINE KINASE RECEPTORS, CONCOMITANTLY RECRUITS ERBB1 AND ERBB2 CORECEPTORS, RESULTING IN LIGAND-STIMULATED TYROSINE PHOSPHORYLATION AND ACTIVATION OF THE ERBB RECEPORS. MAY PLAY AN IMPORTANT ROLE IN PROVIDING GROWTH ADVANTAGE IN NEOPLASTIC CELLS.			
15	92.5	33.4	2192	5	001768	CC -1- SUBUNIT: THE CYTOSMATIC DOMAIN INTERACTS WITH THE LIM DOMAIN REGION OF LIMK1 (BY SIMILARITY).			
16	91.5	33.0	1213	13	090Y54	CC -1- SUBCELLULAR LOCATION: EXISTS AS TYPE I MEMBRANE PROTEIN AND AS A PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE MEMBRANE-BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).			
						CC -1- ALTERNATIVE PRODUCTS: DIFFERENT ISOFORMS ARE PRODUCED BY ALTERNATIVE SPlicing. THE SEQUENCE SHOWN IS THAT OF ISOFORM ALPHA2B/CLONE PM3.			
						CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGHER LEVEL AFTER NEOPLASTIC TRANSFORMATION OF CELLS.			
						CC -1- DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION			





09ESA7 ID 09ESA7 PRELIMINARY; PRT; 136 AA.  
 AC 09ESA7; PRT; 136 AA.  
 DT 01-MAR-2001 (TREMBREL, 16, Created)  
 DT 01-MAR-2001 (TREMBREL, 16, Last sequence update)  
 DT 01-DEC-2001 (TREMBREL, 19, Last annotation update)  
 DE SMDF NEUREGULIN BETA 4 (FRAGMENT).  
 GN NRG1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TAXID=10116; [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RC TISSUE=AKTOMIZED LUMBAR DORSAL ROOT GANGLION/SPINAL CORD;  
 RT \*Structural and Functional Diversity of SMDF Neuregulin Splice Variants Expressed in the Adult Rat Nervous System.;  
 RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF194412; AAC28431; 1; -.  
 DR HSSP: Q12784; IHRP.  
 DR InterPro: IPRO00561; EGF-LIKE.  
 DR Pfam: PF00008; EGF; 1.  
 DR SMART: SM00081; EGF; 1.  
 DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
 FT NON\_TER 136 136  
 SQ SEQUENCE 136 AA: 15235 MW: 116CBG91D6B8AEFS CRC64;  
 Query Match 37.0%; Score 102.5; DB 11; Length 136;  
 Best Local Similarity 31.2%; Pred. No. 1e-06;  
 Matches 15; Conservative 13; Mismatches 19; Indels 1; Gaps 1;  
 FT NON\_TER 1 1  
 OY 1 HFKPCCRDIDAYCLNDGECFVIELTIGSHKH-CRCCEGYYCVRCDQFL 47  
 DB 54 HLTKCAERKTFCVNGGECFTVKDLSNSPRLCKCPNEFTGDRQNYV 101  
 RESULT 8  
 09ESA6 ID 09ESA6 PRELIMINARY; PRT; 256 AA.  
 AC 09ESA6; PRT; 256 AA.  
 DT 01-MAR-2001 (TREMBREL, 16, Created)  
 DT 01-DEC-2001 (TREMBREL, 19, Last sequence update)  
 DE SMDF NEUREGULIN BETA 3 (FRAGMENT).  
 GN NRG1.  
 OS Rattus norvegicus (Rat).  
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OX NCBI\_TAXID=10116; [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RC TISSUE=AKTOMIZED LUMBAR DORSAL ROOT GANGLION/SPINAL CORD;  
 RT \*Structural and Functional Diversity of Glial-Growth Factor Isoforms Expressed in Regenerating Peripheral Nerve and Associated Neurons.;  
 RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF19495; AAC28449; 1; -.  
 DR HSSP: Q12784; IHRP.  
 DR Frohner P.W.; Anderson K.D., Pearson R.J. Jr., InterPro: IPRO00561; EGF-LIKE.  
 DR InterPro: IPRO00885; ER-target.  
 DR InterPro: IPRO003598; IG\_C2.  
 DR InterPro: IPRO03006; IG\_MHC.  
 DR Pfam: PF00047; 19; 1.  
 DR SMART: SM00181; EGF; 1.  
 DR PROSITE: SM0009; IGF; 1.  
 DR SMART: SM00408; IGF2; 1.  
 DR PROSITE: PS00014; ER-TARGET; UNKNOWN\_1.  
 DR KW Immunoglobulin domain.  
 FT NON\_TER 1 317  
 SQ SEQUENCE 317 AA: 34785 MW: 4487FA3E9CD876B9 CRC64;  
 Query Match 37.0%; Score 102.5; DB 11; Length 317;  
 Best Local Similarity 31.2%; Pred. No. 2.5e-06;  
 Matches 15; Conservative 13; Mismatches 19; Indels 1; Gaps 1;  
 FT NON\_TER 1 1  
 OY 1 HFKPCCRDIDAYCLNDGECFVIELTIGSHKH-CRCCEGYYCVRCDQFL 47  
 DB 260 HLTKCAERKTFCVNGGECFTVKDLSNSPRLCKCPNEFTGDRQNYV 307  
 RESULT 10  
 09ESA2 ID 09ESA2 PRELIMINARY; PRT; 323 AA.  
 AC 09ESA2; PRT; 323 AA.  
 DT 01-MAR-2001 (TREMBREL, 16, Created)  
 DT 01-MAR-2001 (TREMBREL, 16, Last sequence update)  
 DT 01-DEC-2001 (TREMBREL, 19, Last annotation update)  
 DR GLIAL GROWTH FACTOR GGF BETA 3 (FRAGMENT).  
 GN NRG1.  
 OS Rattus norvegicus (Rat).  
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OX NCBI\_TAXID=10116; [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RC Carroll S.L., StoneyCypher M.S., Anderson K.D., Pearson R.J. Jr.,  
 RA

Matches 15; Conservative 13; Mismatches 19; Indels 1; Gaps 1;  
 OY 1 HFKPCCRDIDAYCLNDGECFVIELTIGSHKH-CRCCEGYYCVRCDQFL 47  
 DB 193 HLTKCAERKTFCVNGGECFTVKDLSNSPRLCKCPNEFTGDRQNYV 240

RESULT 9

09ESA3

ID 09ESA3 PRELIMINARY; PRT; 317 AA.

AC 09ESA3; PRT; 317 AA.

DT 01-MAR-2001 (TREMBREL, 16, Last sequence update)

DT 01-DEC-2001 (TREMBREL, 19, Last annotation update)

DE GLIAL GROWTH FACTOR GGF BETA 2 (FRAGMENT).

GN NRG1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OC NCBI\_TAXID=10116; [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RC TISSUE=AKTOMIZED LUMBAR DORSAL ROOT GANGLION/SPINAL CORD;  
 RT Carroll S.L., StoneCypher M.S., Anderson K.D., Pearson R.J. Jr.,  
 RA HSSP: Q12784; IHRP.  
 RT Frohner P.W.; Anderson K.D., Pearson R.J. Jr., InterPro: IPRO00561; EGF-LIKE.  
 RT InterPro: IPRO00885; ER-target.  
 DR InterPro: IPRO003598; IG\_C2.  
 DR InterPro: IPRO03006; IG\_MHC.  
 DR Pfam: PF00047; 19; 1.  
 DR SMART: SM00181; EGF; 1.  
 DR PROSITE: SM0009; IGF; 1.  
 DR SMART: SM00408; IGF2; 1.  
 DR PROSITE: PS00014; ER-TARGET; UNKNOWN\_1.  
 DR KW Immunoglobulin domain.  
 FT NON\_TER 1 317  
 SQ SEQUENCE 317 AA: 34785 MW: 4487FA3E9CD876B9 CRC64;  
 Query Match 37.0%; Score 102.5; DB 11; Length 317;  
 Best Local Similarity 31.2%; Pred. No. 2.5e-06;  
 Matches 15; Conservative 13; Mismatches 19; Indels 1; Gaps 1;  
 FT NON\_TER 1 1  
 OY 1 HFKPCCRDIDAYCLNDGECFVIELTIGSHKH-CRCCEGYYCVRCDQFL 47  
 DB 260 HLTKCAERKTFCVNGGECFTVKDLSNSPRLCKCPNEFTGDRQNYV 307

RA Frohnert, P.W.;  
 RT "Structural and Functional Diversity of Glial Growth Factor Isoforms  
 RT Expressed in Regenerating Peripheral Nerve and Associated Neurons.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF194996; AAC28450.1; -.  
 DR HSMP: Q12784; IHE.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR03598; Ig-c2.  
 DR InterPro; IPR03600; Ig-like.  
 DR InterPro; IPR03606; Ig-MHC.  
 PFam: PF00047; Ig.  
 DR SMART; SM00181; EGF; 1.  
 DR SMART; SM00001; EGF-like; 1.  
 DR SMART; SM00049; Ig; 1.  
 DR SMART; SM00048; IgG2; 1.  
 DR SMART; SM00040; IgG2; 1.  
 DR SMART; SM00010; Ig-like; 1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 KW Immunoglobulin domain.  
 FT NON\_TER 1.  
 SQ SEQUENCE 323 AA: 35358 MW: C7DF153A93A80C8 CRC64;

RESULT 11

Query Match 37.0%; Score 102.5; DB 11; Length 323;  
 Best Local Similarity 31.2%; Pred. No. 2.5e-05; Mismatches 15; Indels 1; Gaps 1;  
 Matches 15; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

Qy 1 HFKPCRDLDLAVLNDGECFVLTGSHKH-CRCKEGYQGYRCQDFL 47  
 DB 260 HLIKCAEKEKTFCVNGECFTVKDLSPRSVRLCKCPNEFTGDRCONV 307

Q9ESB1 ID Q9ESB1 PRELIMINARY; PRT; 700 AA.

AC Q9ESB1; 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE SMDF NEUREGULIN BETA 1A.  
 GN NRG1.  
 OS Rattus norvegicus (Rat).  
 OC Bukarjota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN NCBI\_TaxID-10116; [1]

RP SEQUENCE FROM N.A.

RC STRAIN-SPRAGUE-DAWLEY;

RA Carroll, S.L., Anderson, K.D., Frohnert, P.W.;  
 RT "Structural and Functional Diversity of SMDF Neuregulin Splice  
 Variants Expressed in the Adult Rat Nervous System.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF194438; AAC8427.1; -.  
 DR HSSP: Q12784; IHE.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR002154; Neuregulin.  
 DR InterPro; IPR002114; PTS\_HPr\_ser.  
 DR Pfam: PF00008; EGF; 1.  
 DR Pfam; PF02158; Neuregulin; 1.  
 DR PRIMs; PR01089; NEUREGULIN.  
 DR SMART; SM00181; EGF; 1.  
 DR SMART; SM00001; EGF-like; 1.  
 DR PROSITE; PS00589; PTS\_HPr\_SER; UNKNOWN\_1.  
 SQ SEQUENCE 700 AA; 76386 MW: 2F811817ECC49DA CRC64;

RESULT 12

Query Match 37.0%; Score 102.5; DB 11; Length 700;  
 Best Local Similarity 31.2%; Pred. No. 5.7e-06; Mismatches 15; Indels 1; Gaps 1;  
 Matches 15; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

Qy 1 HFKPCRDLDLAVLNDGECFVLTGSHKH-CRCKEGYQGYRCQDFL 47  
 DB 234 HLIKCAEKEKTFCVNGECFTVKDLSPRSVRLCKCPNEFTGDRCONV 281

Q9ESAS ID Q9ESAS PRELIMINARY; PRT; 782 AA.

AC Q9ESAS; 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE GLIAL GROWTH FACTOR BETA 1A (FRAGMENT).  
 GN NRG1.  
 OS Rattus norvegicus (Rat).  
 OC Bukarjota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN NCBI\_TaxID-10116; [1]

RP SEQUENCE FROM N.A.

RC STRAIN-SPRAGUE-DAWLEY; TISSUE-SPINAL CORD/BRAIN STEM;

RA Carroll, S.L., Stoenecypher, M.S., Anderson, K.D., Pearson, R.J. Jr.,  
 RT "Structural and Functional Diversity of Glial Growth Factor Isoforms  
 RT Expressed in Regenerating Peripheral Nerve and Associated Neurons.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF194997; AAC28451.1; -.  
 DR HSSP: Q12784; IHE.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR003598; Ig-c2.  
 DR InterPro; IPR003006; Ig-MHC.  
 DR PFam: PF00047; Ig.  
 DR SMART; SM00181; EGF; 1.  
 DR SMART; SM00001; EGF-like; 1.  
 DR SMART; SM00409; Ig; 1.  
 DR SMART; SM00408; IgG2; 1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 KW Immunoglobulin domain.  
 FT NON\_TER 1.  
 SQ SEQUENCE 342 AA; 37836 MW: 88E36FC836553124 CRC64;

Query Match 37.0%; Score 102.5; DB 11; Length 342;  
 Best Local Similarity 31.2%; Pred. No. 2.7e-06; Mismatches 15; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

Matches 15; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

RA Frohnert, P.W.;  
 RT "Structural and Functional Diversity of Glial Growth Factor Isoforms  
 RT Expressed in Regenerating Peripheral Nerve and Associated Neurons.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF194993; AAC28433.1; -.  
 DR HSSP: Q12784; IHE.  
 DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR003598; Ig\_c2.

DR InterPro; IPR03005; Ig\_MIC.

DR InterPro; IPR02154; Neuregulin.

DR InterPro; IPR02114; prs\_Hpr\_ser.

DR Pfam; PF00047; Ig; 1.

DR Pfam; PF02158; Neuregulin; 1.

DR Prints; PRO1089; NEURREGULIN.

DR SMART; SM00181; EGF; 1.

DR SMART; SM00011; EGF\_like; 1.

DR SMART; SM00409; Ig; 1.

DR SMART; SM00408; IGC2; 1.

DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.

DR PROSITE; PS00589; prs\_Hpr\_SER; UNKNOWN\_1.

KW Immunoglobulin domain.

FT NON\_TER 1

SQ .SEQUENCE 782 AA; 86036 MW; F6174A68P4E27BDE CRC64;

Query Match 37.0%; Score 102.5; DB 11; Length 782;

Best Local Similarity 31.3%; Pred. No. 6.5e-06;

Matches 15; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

OY 1 HFKPCRDIDAYCLNDGECFVIELTIGSHK-CRCKEGQYQGRQDQFL 47

-Db 316 HLIKCAKEKTCFVNGEFTVKDLSNPRLKCPNFTGDRQMV 363

RESULT 14

Q91M20 PRELIMINARY; PRT; 89 AA.

ID Q91M20; PRELIMINARY; PRT; 89 AA.

AC Q91M20; PRELIMINARY; PRT; 89 AA.

DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DE LSDV016 EGF-LIKE GROWTH FACTOR.

GN LSDV016.

OS lumpy skin disease virus.

OC Vitaceae; dsDNA viruses; no RNA stage; Poxviridae; Chordopoxvirinae;

OC Capripoxvirus.

OX NCBI\_TAXID=55509;

RP [1]

SEQUENCE FROM N.A.

RC STRAIN=NZETHLING\_2490;

RX MEDLINE=21320495; PubMed=11435593;

RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.;

RT "Genome of lumpy skin disease virus.";

RL J. Virol. 75:7122-7130(2001).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=NZETHLING\_2490;

RX MEDLINE=21320495; PubMed=11435593;

RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.;

RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL; AP32528; NAR4977.1; LSDV016.

SQ SEQUENCE 89 AA; 10646 MW; 1D5F3FD7D06174E0 CRC64;

Query Match 35.7%; Score 99; DB 12; Length 89;

Best Local Similarity 43.9%; Pred. No. 2e-06; Mismatches 18; Conservative 6; Indels 4; Gaps 1;

OY 7 DKDLCYCLNDGECFVIELTIGSHK---HCKEGQYQGRQ 43

-Db 40 DKSINFLNGGCKYTFILSYNNKKLMLFCCKLGEGVQC 80

RESULT 15

Q01768 PRELIMINARY; PRT; 2192 AA.

ID Q01768; PRELIMINARY; PRT; 2192 AA.

AC Q01768; PRELIMINARY; PRT; 2192 AA.

DT 01-JUL-1997 (Tremblrel. 04, Created)

DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE HYPOTHETICAL 242.7 KDA PROTEIN.

GN T21E3.3.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nemata; Chromadorea; Rhabditida; Rhabditoldea;

OC Rhabditidae; Peioderinae; Caenorhabditis.

OX NCBI\_TAXID=6239;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RX MEDLINE=99069613; PubMed=9851916;

RA None;

RT "Genome sequence of the nematode *C. elegans*: a platform for investigating biology. The *C. elegans* Sequencing Consortium.";

RT Science 282:2012-2018(1998).

[2]

RA Du Z.; Le T.T.; STRAIN=BRISTOL N2;

RT SEQUENCE FROM N.A.

RA SEQUENCE FROM N.A.

RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RA Waterston R.;

RT "Direct Submission"; Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF003133; AAB54138.2;

DR HSPB; 007954; 1KB8.

DR InterPro; IPR00561; EGF-like.

DR InterPro; IPR003049; Laminin EGF.

DR InterPro; IPR00033; LDL\_receptor\_rep.

DR Pfam; PF00008; EGF; 8.

DR InterPro; IPR002049; Ldl\_recept\_a.

DR Pfam; PF00057; ldl\_recept\_a; 18.

DR InterPro; IPR002172; Ldl\_recept\_A.

DR Prints; PRO0011; EGFAMININ.

DR Prints; PRO0021; LDLRECEPTPHOR.

DR SMART; SM00181; EGF; 23.

DR SMART; SM00192; LDL; 18.

DR SMART; SM00135; LY; 7.

DR PROSITE; PS00022; EGF\_1; UNKNOWN\_9.

DR PROSITE; PS01186; EGF\_2; 7.

DR PROSITE; PS01209; LDLRA\_1; 10.

DR PROSITE; PS50008; LDLRA\_2; 12.

DR KW EGF-like domain; Glycoprotein; Hypothetical protein.

SQ SEQUENCE 2192 AA; 242666 MW; F47625EBCB45BDA CRC64;

Query Match 33.4%; Score 92.5; DB 5; Length 2192;

Best Local Similarity 42.9%; Pred. No. 0.00049; Mismatches 18; Conservative 8; Indels 9; Gaps 3;

OY 5 CRDKLCYCLNDGECFVIELTIGSHK---HCKEGQYQGRQ 45

-Db 1918 CDD---YC7NNSKC---TITNGTHFBCDKKGFKGLRCE 1951

Search completed: November 7, 2002, 10:02:59

Job time : 27 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 7, 2002, 09:59:08 ; Search time 11 Seconds  
(without alignments)  
165.438 Million cell updates/sec

Title: US-09-480-977-4  
Perfect score: 277

Sequence: 1 HFKCQCDKQDLYCINDEGF.....SHKHCRCCKEGYQQVRCDOFL 47

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	277	100.0	713	1	NRG3_MOUSE	035181	NRG3_MOUSE STANDARD; PRT; 713 AA.
2	277	100.0	720	1	NRG3_HUMAN	035181	NRG3_HUMAN (Rel. 40, Created)
3	126.5	45.7	677	1	NRG1_XENLA	022979	NRG1_XENLA (Rel. 40, Last sequence update)
4	113.5	41.0	639	1	NRG1_HUMAN	022979	NRG1_HUMAN (Rel. 40, Last annotation update)
5	110	39.7	115	1	NRG4_MOUSE	09wt24	NRG4_MOUSE (Rel. 40, Last annotation update)
6	104.5	37.7	296	1	SIDE_HUMAN	015191	SIDE_HUMAN (Rel. 40, Last annotation update)
7	104	37.5	296	1	NRG2_MOUSE	056914	NRG2_MOUSE (Rel. 40, Last annotation update)
8	102.5	37.0	662	1	NRG1_RAT	P43322	NRG1_RAT (Rel. 40, Last annotation update)
9	98.5	35.6	602	1	NRG1_CHICK	005199	NRG1_CHICK (Rel. 40, Last annotation update)
10	90	32.5	850	1	NRG2_HUMAN	014510	NRG2_HUMAN (Rel. 40, Last annotation update)
11	90	32.5	868	1	NRG2_RAT	035369	NRG2_RAT (Rel. 40, Last annotation update)
12	89.5	32.3	169	1	NRG1_HUMAN	014944	NRG1_HUMAN (Rel. 40, Last annotation update)
13	85	30.7	80	1	GRFA_SWINKA	P08441	GRFA_SWINKA (Rel. 40, Last annotation update)
14	83	30.0	2531	1	NRG1_MOUSE	P01705	NRG1_MOUSE (Rel. 40, Last annotation update)
15	82.5	29.8	177	1	BTC_MOUSE	005028	BTC_MOUSE (Rel. 40, Last annotation update)
16	82	29.8	178	1	BTC_BOVIN	09tcc5	BTC_BOVIN (Rel. 40, Last annotation update)
17	82	29.6	85	1	GRFA_MXVL	P08072	GRFA_MXVL (Rel. 40, Last annotation update)
18	82	29.6	230	1	SPIT_DROME	001083	SPIT_DROME (Rel. 40, Last annotation update)
19	80.5	29.1	125	1	V211_POMPV	Q9J524	V211_POMPV (Rel. 40, Last annotation update)
20	80.5	29.1	178	1	BTC_HUMAN	P35070	BTC_HUMAN (Rel. 40, Last annotation update)
21	79.5	28.7	140	1	GRFA_YACCV	P01036	GRFA_YACCV (Rel. 40, Last annotation update)
22	79.5	28.7	142	1	GRFA_VACCV	P20494	GRFA_VACCV (Rel. 40, Last annotation update)
23	79.5	28.7	159	1	TGFLA_MOUSE	P48030	TGFLA_MOUSE (Rel. 40, Last annotation update)
24	79.5	28.7	159	1	TGFA_RAT	P01134	TGFA_RAT (Rel. 40, Last annotation update)
25	79	28.5	2531	1	NTCL1_RAT	Q07008	NTCL1_RAT (Rel. 40, Last annotation update)
26	78	28.2	1207	1	EGF_HUMAN	P01133	EGF_HUMAN (Rel. 40, Last annotation update)
27	77.5	28.0	714	1	DLL1_RAT	P97677	DLL1_RAT (Rel. 40, Last annotation update)
28	77.5	28.0	722	1	DLL1_MOUSE	061483	DLL1_MOUSE (Rel. 40, Last annotation update)
29	76	27.4	484	1	LEM2_PIG	P98110	LEM2_PIG (Rel. 40, Last annotation update)
30	76	27.4	1217	1	EGF_MOUSE	P01132	EGF_MOUSE (Rel. 40, Last annotation update)
31	76	27.4	12139	1	CRB_DROME	P01040	CRB_DROME (Rel. 40, Last annotation update)
32	75	27.1	611	1	LEM2_CANPA	P37730	LEM2_CANPA (Rel. 40, Last annotation update)
33	74.5	26.9	603	1	FR12_CAVPO	Q04962	FR12_CAVPO (Rel. 40, Last annotation update)

### ALIGNMENTS

34	74.5	26.9	723	1	DLL1_HUMAN	00548	homo sapien
35	74.5	26.9	1429	1	L112_CABEL	P14585	caenorhabditis elegans
36	74	26.7	551	1	LEM2_RABBIT	P27113	oryctolagus cuniculus
37	74	26.7	610	1	LEM2_HUMAN	P16581	homo sapien
38	74	26.7	2871	1	FBN1_BOVIN	P38133	bos taurus
39	74	26.7	2871	1	FBN1_HUMAN	P35555	homo sapien
40	74	26.7	2871	1	FBN1_MOUSE	061554	mus musculus
41	74	26.7	2871	1	FBM1_PIG	09tj56	sus scrofa
42	73	26.4	294	1	GRK2_DROME	P42287	drosophila melanogaster
43	73	26.4	409	1	MGRK1_PIG	P79385	sus scrofa
44	73	26.4	1964	1	NRG4_MOUSE	P31695	mus musculus
45	73	26.4	2524	1	NOTC_XENLA	P21783	xenopus laevis

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CC

CC EMBL; AF010130; ABT70914.1; -.

CC MGD; MGI:1097165; Nrg3.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR002154; Neuregulin.

DR Pfam; PF00008; EGF; 1.

DR SMART; SM00181; EGF; 1.

DR PROSITE; PS00022; EGF\_1; 1.

DR PROSITE; PS01186; EGF\_2; 1.

KW Growth factor; EGF-like domain; transmembrane; Multigene family.

FT CHAIN 1 713 PRO-NEUREGULIN-3; MEMBRANE-BOUND FORM.

FT CHAIN 1 361 NEUREGULIN-3.

FT DOMAIN 1 362 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 363 383 INTERNAL SIGNAL SEQUENCE (POTENTIAL).

FT DOMAIN 384 713 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 105 287 SER/THR-RICH.

FT DOMAIN 288 331 EGF-LIKE.

FT DOMAIN 13 21 POLY-ALA.

FT DOMAIN 26 34 POLY-ALA.

FT DOMAIN 127 135 POLY-THR.

FT DOMAIN 250 253 POLY-ALA.

FT DOMAIN 254 263 POLY-SER.

FT DOMAIN 264 267 POLY-THR.

FT DISULFID 292 306 BY SIMILARITY.

FT DISULFID 300 319 BY SIMILARITY.

FT DISULFID 321 330 BY SIMILARITY.

SO SEQUENCE 713 AA; 77369 MW; 9F7D1D5E/FC8DC0F0 CRC64;

Query Match 100.0%; Score 277; DB 1; Length 713;

Best Local Similarity 100.0%; Pred. No. 5. 9e-26;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HKPKCRDKDYLAYCLNDGECFVIEPTLGSHKHCRCKEGYQSVRCDFL 47

Db 288 HKPKCRDKDYLAYCLNDGECFVIEPTLGSHKHCRCKEGYQSVRCDFL 334

RESULT 2

NRG3\_HUMAN STANDARD; PRT; 720 AA.

ID NRG3\_HUMAN STANDARD; PRT; 720 AA.

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pro-neuregulin-3 Precursor (Pro-NRG3) [Contains: Neuregulin-3 (NRG-3)].

GN NRG3.

OS Homo sapiens (Human).

OC Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

NCBI\_TAXID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Fetal brain;

RA MEDLINE-97420720; Pubmed-275162;

RA Zhang D., Sliwkowski M.X., Mark M., Frantz G., Akita R., Sun Y., Hiltan K., Crowley C., Brush J., Godowski P.J.;

RA "Neuregulin-3 (NRG3): a novel neural tissue-enriched protein that binds and activates ErbB4.";

RA PROC. NATL. ACAD. SCI. U.S.A. 94:9562-9567 (1997).

CC 1- FUNCTION: DIRECT LIGAND FOR THE ERBB4 TYROSINE KINASE RECEPTOR.

CC BINDING RESULTS IN LIGAND-STIMULATED TYROSINE PHOSPHORYLATION AND ACTIVATION OF THE RECEPTOR. DOES NOT BIND TO THE EGF RECEPTOR, ERBB2 OR ERBB3 RECEPTORS.

CC -1- SUBCELLULAR LOCATION: EXISTS AS AN TYPE I MEMBRANE PROTEIN AND AS A PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR AND AS MEMBRANE-BOUND FORM. DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).

CC TISSUE SPECIFICITY: HIGHLY EXPRESSED IN MOST REGIONS OF THE BRAIN WITH THE EXCEPTION OF CORPUS CALLOSUM. EXPRESSED AT LOWER LEVEL IN TESTIS. NOT DETECTED IN HEART, PLACENTA, LUNG, LIVER, SKELETAL

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CC

CC MUSCLE, KIDNEY, PANCREAS, SPLEEN, THYMUS, PROSTATE, OVARY, SMALL INTESTINE, COLON AND PERIPHERAL BLOOD LEUKOCITES.

CC -1- DOMAIN: THE CYTOSLAMIC DOMAIN MAY BE INVOLVED IN THE REGULATION OF TRAFFICKING AND PROTEOLYTIC PROCESSING. REGULATION OF THE PROTEOLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN.

CC DIMERIZATION (BY SIMILARITY).

CC -1- DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE DOMAIN (BY SIMILARITY).

CC -1- PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR FORM (BY SIMILARITY).

CC -1- PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE (BY SIMILARITY).

CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

CC -1- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.

DR MM; 60553;

DR InterPro; IPR000561; EGF-like.

DR PROSITE; PS00022; EGF\_1; 1.

KW Growth factor; EGF-like domain; transmembrane; Multigene family.

FT CHAIN 1 720 PRO-NEUREGULIN-3; MEMBRANE-BOUND FORM.

FT DOMAIN 1 359 NEUREGULIN-3.

FT DOMAIN 1 360 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 361 381 INTERNAL SIGNAL SEQUENCE (POTENTIAL).

FT DOMAIN 382 720 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 105 285 SER/THR-RICH.

FT DOMAIN 286 329 EGF-LIKE.

FT DOMAIN 5 8 POLY-ALA.

FT DOMAIN 21 21 POLY-ALA.

FT DOMAIN 34 34 POLY-ALA.

FT DOMAIN 127 135 POLY-THR.

FT DOMAIN 252 260 POLY-SER.

FT DISULFID 290 304 POLY-THR.

FT DISULFID 298 317 BY SIMILARITY.

FT DISULFID 319 328 BY SIMILARITY.

SO SEQUENCE 720 AA; 77900 MW; AAD6F10DB95A693 CRC64;

Query Match 100.0%; Score 277; DB 1; Length 720;

Best Local Similarity 100.0%; Pred. No. 5. 9e-26;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HKPKCRDKDYLAYCLNDGECFVIEPTLGSHKHCRCKEGYQSVRCDFL 47

Db 286 HKPKCRDKDYLAYCLNDGECFVIEPTLGSHKHCRCKEGYQSVRCDFL 332

RESULT 3

NRG1\_XENLA STANDARD; PRT; 677 AA.

ID NRG1\_XENLA STANDARD; PRT; 677 AA.

AC O93383; O9W640;

AC DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pro-neuregulin-1 precursor (Pro-NRG1) [Contains: Neuregulin-1].

GN NRG1.

OS Xenopus laevis (African clawed frog).

OS Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Barracchii; Anura; Mesobatrachia; Pipidae;

OC Xiphopoda; Xenopus.

OC NCBI\_TAXID=8355;

RP SEQUENCE FROM N.A. (ISOFORM ALPHAI), AND ALTERNATIVE SPLICING.

RA MEDLINE-9832126; Pubmed-3685555;

RA Yang J.-P., Zhou H., Pun S., IP N.Y., Peng H.-B., Tsim K.W.K.;

RA "Cloning of cDNAs encoding xenopus neuregulin: expression in myotomal muscle during embryo development.";

RA Brain Res. Mol. Brain Res. 58:59-73 (1998).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM CRD).





DR	PROSITE: PS01186; EGF-2; 1.
KW	Growth factor; EGF-like domain; Immunoglobulin domain; Glycoprotein; Transmembrane; Multigene family; Polymorphism; 3D-structure;
KW	Alternative splicing; Chromosomal translocation.
QY	1 HFRPCRDKDLYCLNDCECFVTEITLGSKH-CCKCEGQYQGRQDQ 45
Db	177 HLVCKCERKETFCVNGGCEFMVKDLSNPSRYLCKCOPGFTGARCTE 222
RESULT 5	
NRG4_MOUSE	Best Local Similarity 41.0%; Score 113.5; DB 1; Length 639;
STANDARD:	PRT; 115 AA.
ID	NRG4_MOUSE
AC	Q9W7X4;
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	01-MAR-2002 (Rel. 41, Last annotation update)
DE	Pro-neuregulin-4, short isoform (Pro-NRG4) (Contains: Neuregulin-4 (NRG-4)).
DE	GN
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBL_TaxID-10990;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C7BL/6J; TISSUE=Liver;
RX	MEDLINE=>9276598; PUBMED=10348342;
RA	Harari D., Tzahar E., Romano J., Shelly M., Pierce J.H., Andrews G.C.,
RA	Yarden Y.;
RT	-1- Neuregulin-4: a novel growth factor that acts through the Erbb-4 receptor tyrosine kinase.;
RT	-1- SUBCELLULAR LOCATION: EXISTS AS AN TYPE I MEMBRANE PROTEIN AND AS A PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE MEMBRANE-BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).
CC	-1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS MAY BE PRODUCED BY ALTERNATIVE SPLICING.
CC	-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PANCREAS; WEAKLY EXPRESSED IN MUSCLE.
CC	-1- DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION OF TRAFFICKING AND PROTEOLYTIC PROCESSING. REGULATION OF THE PROTEOLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN DIMERIZATION (BY SIMILARITY).
CC	-1- DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE DOMAIN (BY SIMILARITY).
CC	-1- PTM: PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR (BY SIMILARITY).
CC	-1- PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE (BY SIMILARITY).
CC	-1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC	-1- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.
CC	-----
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CC	-----
CC	EMBL: AF083067; AAD21874.1; -
CC	MGD: MG1:193383; Nrg4.
DR	PROSITE: PS00022; EGF-1; 1.
DR	PROSITE: PS01186; EGF-2; FALSE, NEG.
KW	Growth factor; EGF-like domain; Glycoprotein; Transmembrane; Multigene family; Alternative splicing.
FT	CHAIN 1 115 PRO-NEUREGULIN-4, MEMBRANE-BOUND FORM.
FT	CHAIN 1 61 NEUREGULIN-4.
FT	DOMAIN 1 62 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 63 INTERNAL SIGNAL SEQUENCE (POTENTIAL).
FT	DOMAIN 84 115 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 5 46 EGF-LIKE.
FT	DISULFID 9 23 BY SIMILARITY.
FT	DISULFID 17 34 BY SIMILARITY.
FT	DISULFID 36 45 BY SIMILARITY.
FT	CARBOHYD 39 39 N-LINKED (GLCNAC, . . .) (POTENTIAL).
FT	CARBOHYD 60 60 N-LINKED (GLCNAC, . . .) (POTENTIAL).
SQ	SEQUENCE 115 AA; 12743 MW; 989AE376857BA9 Crc64;
RESULT 6	
SMDF_HUMAN	Best Local Similarity 42.2%; Score 110; DB 1; Length 115;
STANDARD:	PRT; 296 AA.
ID	SMDF_HUMAN
AC	Q15491;
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DE	Neuregulin-1, sensory and motor neuron-derived factor isoform.
DE	NRG1 OR HGL OR RHPA OR HRG A OR GGF OR SMDF.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBL_TaxID-9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Brain stem, and Cerebellum;
RX	MEDLINE=>9501514; PubMed=772315;
RA	Ho W.H., Armanini M.P., Nijhuis A., Phillips H.S., Osheroff P.L.,
CC	*Sensory and motor neuron-derived factor. A novel heregulin variant
CC	RT highly expressed in sensory and motor neurons.;
RL	J. Biol. Chem. 270:4523-1452 (1995).
CC	-1- FUNCTION: THE ISOFORM SMDF MAY PLAY A ROLE IN MOTOR AND SENSORY NEURON DEVELOPMENT.
CC	-1- SUBCELLULAR LOCATION: SECRETED. MAY POSSESS AN INTERNAL UNCLEAVED SIGNAL SEQUENCE.
CC	-1- ALTERNATIVE PRODUCTS: AT LEAST 10 ISOFORMS OF NRG1 ARE PRODUCED BY ALTERNATIVE SPlicing. EXCEPT FOR SMDF THEY ARE IN ENTRY AC Q02297.
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN NERVOUS SYSTEM: SPINAL CORD MOTOR NEURONS, DORSAL ROOT GANGLION NEURONS, AND BRAIN. PREDOMINANT ISOFORM EXPRESSED IN SENSOR AND MOTOR NEURONS. NOT DETECTED IN ADULT HEART, PLACENTA, LUNG, SKELLET MUSCLE, KIDNEY, AND PANCREAS. NOT EXPRESSED IN FETAL LUNG, LIVER, AND KIDNEY.
CC	-1- DEVELOPMENTAL STAGE: HIGHLY EXPRESSED IN DEVELOPING SPINAL MOTOR NEURONS AND IN DEVELOPING CRANIAL NERVE NUCLEI. EXPRESSION IS MAINTAINED ONLY IN BOTH ADULT MOTOR NEURONS AND DORSAL ROOT GANGLION NEURONS.
CC	-1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC	-1- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.
CC	-----
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DR EMBL: LA1827; AAC1764; 1;  
 DR HSRP: 012784; 1HRE.  
 DR MIM: 14445; -;  
 DR InterPro: IPR00561; EGF-like.  
 DR Pfam: PF0008; EGF; 1.  
 DR SMART: SM00181; EGF; 1.  
 DR PROSITE: PS00022; EGF; 1; 1.  
 DR PROSITE: PS01186; EGF; 2; 1.  
 DR KW Growth factor; EGF-like domain; transmembrane; Multigene family;  
 KW Alternative splicing.  
 FT TRANSMEM 76 100 INTERNAL SIGNAL SEQUENCE (POTENTIAL).  
 FT DOMAIN 58 91 CIS-RICH.  
 FT DOMAIN 211 232 SER/THR-RICH.  
 FT DOMAIN 233 277 EGF-LIKE.  
 FT DISULFID 237 251 BY SIMILARITY.  
 FT DISULFID 245 265 BY SIMILARITY.  
 FT DISULFID 267 276 BY SIMILARITY.  
 CC SEQUENCE 296 AA; 31685 MW; 8D41743217F7EB02 CRC64;

Query Match 37.7%; Score 104.5; DB 1; Length 295;  
 Best Local Similarity 31.2%; Pred. No. 1.3e-05; Matches 15; Conservative 14; Mismatches 18; Indels 1; Gaps 1;

QY 1 HFKPCRDKDLYCLNLDGECVFIETLGSNH-HCRKEGYQVRCDOFL 47  
 Db 233. HFKCQEKEKTFCVNGECFVKDLSNPRLCKPNEFGDRCONVY 280

RESULT 7

NRG2\_MOUSE STANDARD; PRT; 756 AA.

ID NRG2\_MOUSE STANDARD; PRT; 756 AA.

AC P56971; 1  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Pro-neuregulin-2 precursor (Pro-NRG2) [Contains: Neuregulin-2 (NRG-2)]  
 DE (Divergent of neuregulin 1) (DON-1).  
 GN NRG2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TAXID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS NRG2-5; NRG2-10 AND NRG2-16A).  
 RC STRAIN="C57BL/6, TISSUE=Brain"; MEDLINE="91311398; PubMed=916815;  
 RC Carraway K.L. III, Weber J.L., Unger M.J., Ledesma J., Yu N.,  
 RC Gassmann M., Lai C.;  
 RT "Neuregulin-2, a new ligand of Erbb3/Erbb4-receptor tyrosine  
 RT kinases." Nature 387:512-516(1997).  
 RN [2]  
 RP SEQUENCE OF 150-756 FROM N.A. (ISOFORMS DON-1M AND DON-1S).  
 RC TISSUE="Choroid plexus"; MEDLINE="9734238; PubMed=919335;  
 RC Busfield S.J., Michnick D.A., Chickerling T.W., Revett T.L., Ma J.,  
 RA Woolf E.A., Comrack C.A., Dussault B.J., Wolf J., Goodearl A.D.J.,  
 RA Gearing D.P.;  
 RT "Characterization of a neuregulin-related gene, Don-1, that is highly  
 RT expressed in restricted regions of the cerebellum and hippocampus." Mol.  
 RL Cell. Biol. 17:4007-4014(1997).  
 CC -1- FUNCTION: DIRECT LIGAND FOR ERBB3 AND ERBB4 TYROSINE KINASE  
 CC RECEPTORS. CONCOMITANTLY RECRUITS ERBB1 AND ERBB2 CORECEPTORS,  
 CC RESULTING IN LIGAND-STIMULATED TYROSINE PHOSPHORYLATION AND  
 CC ACTIVATION OF THE ERBB RECEPTORS. MAY ALSO PROMOTE THE  
 CC HETERO-DIMERIZATION WITH THE EGF RECEPTOR.  
 CC -1- SUBCELLULAR LOCATION: EXISTS AS AN TYPE I MEMBRANE PROTEIN AND AS  
 CC A PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE

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CC DR EMBL: LA1827; AAC1764; 1;  
 CC DR HSRP: 012784; 1HRE.  
 CC DR MIM: 14445; -;  
 CC DR InterPro: IPR00561; EGF-like.  
 CC DR Pfam: PF0008; EGF; 1.  
 CC DR SMART: SM00181; EGF; 1.  
 CC DR PROSITE: PS00022; EGF; 1; 1.  
 CC DR PROSITE: PS01186; EGF; 2; 1.  
 CC DR KW Growth factor; EGF-like domain; immunoglobulin domain; Glycoprotein;  
 KW Transmembrane; Multigene family; Alternative splicing.  
 FT PROTEP 1 BY SIMILARITY.  
 FT CHAIN 20 756 PRO-NEUREGULIN-2, MEMBRANE-BOUND FORM.  
 FT DOMAIN 20 314 NEUREGULIN-2.  
 FT TRANSMEM 316 336 INTERNAL SIGNAL SEQUENCE (POTENTIAL).  
 FT DOMAIN 337 755 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 158 226 IG-LIKE C2-TYPE DOMAIN.  
 FT DOMAIN 238 248 SER/THR-RICH.  
 FT DOMAIN 249 290 EGF-LIKE.  
 FT DISULFID 627 633 POLY-PRO.  
 FT DISULFID 165 219 BY SIMILARITY.  
 FT DISULFID 253 267 BY SIMILARITY.  
 FT DISULFID 261 278 BY SIMILARITY.  
 FT CARBOHYD 280 289 BY SIMILARITY.  
 FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 296 296 C->G (IN ISOFORM NRG2-10).  
 FT VARSPLC 280 280 MISSING (IN ISOFORM NRG2-10).  
 FT VARSPLC 281 281 MISSING (IN ISOFORM NRG2-10).  
 FT VARSPLC 282 282 VGYTGSRCQFQAMVWNSKHLGFEELAEELVQKVLITGQ  
 FT VARSPLC 283 330 CVALWVG-> NGFFQRCLEKPLRIMDPKPSVLMWT  
 FT VARSPLC 331 756 PGIVGASSQWSTSPSLDN (IN ISOFORM DON-1S).  
 FT VARSPLC 282 307 VGYTGSRCQFQAMVWNSKHLGFEELAEELVQKVLITGQ  
 FT VARSPLC 308 510 LPLRLIMDPKQ (IN ISOFORM DON-1M).  
 SQ SEQUENCE 756 AA; 82213 MW; 5105DC918BE678E CRC64;

Query Match 37.5%; Score 104; DB 1; Length 756;  
 Best Local Similarity 39.1%; Pred. No. 3.7e-05; Matches 18; Conservative 8; Mismatches 18; Indels 2; Gaps 1;

QY 1 HFKPCRDKDLYCLNLDGECVFIETLGSNH-HCRKEGYQVRCDOFL 46  
 Db 249 HARKCNETAKSYCVNGCVYIEGI-> NOLSCKCPVGVYGDRCQF 292

RESULT 8  
 NRGL\_RAT

**ID** NRG1\_RAT STANDARD PRT; 662 AA.  
**AC** P43322; P43323; P43325; P43326; P43327; P43328;  
**DT** 16-OCT-2001 (Rel. 40, created)  
**DT** 16-OCT-2001 (Rel. 40, last sequence update)  
**DT** 16-OCT-2001 (Rel. 40, last annotation update)  
**DE** differentiatin factor (Heregulin) (HRG) (Contains: Neuregulin-1 (Neu  
**DE** Inducing activity) (ARIA) (Sensory and motor neuron-derived factor)  
**DE** (Gial growth factor)).  
**GN** NRG1 OR NDF.  
**OS** Rattus norvegicus (Rat).  
**OC** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteostomi;  
**OX** Mammalia; Eutheria; Rodentia; Sciuromathi; Muridae; Murinae; Rattus.  
**RN** NERI\_TOXID-10116;  
**RP** TISSUE-Fibroblast;  
**RC** TISSUE-Fibroblast;  
**RX** MEDLINE-94158863; PubMed-5709448;  
**RA** Wen D., Suggs S.V., Karunagaran D., Liu N., Cupples R.L., Luo Y.,  
**RA** Janssen A.M., Ben-Baruch N., Trolinger D.B., Jacobsen V.L.,  
**RA** Meng S.-Y., Lu H.-S., Hu S., Chang D., Yang W., Yanigahara D.,  
**RA** Koski R.A., Yarden Y.;  
**RT** "Structural and functional aspects of the multiplicity of Neu  
**RT** differentiation factors";  
**RL** Mol. Cell. Biol. 14:1909-1919 (1994).  
**RN** [12]  
**RP** SEQUENCE FROM N.A. (ISOFORM ALPHA2C/NDF44), AND PARTIAL SEQUENCE.  
**RC** TISSUE-Fibroblast;  
**RX** MEDLINE-92257596; PubMed-1349853;  
**RA** Wen D., Peles E., Cupples R., Suggs S.V., Bacus S.S., Luo Y.,  
**RA** Trail G., Hu S., Silbiger S.M., Levy R.B., Koski R.A., Lu H.S.,  
**RA** Yarden Y.;  
**RT** "Neu differentiation factor: a transmembrane glycoprotein containing  
**RT** an EGF domain and an immunoglobulin homology unit";  
**RL** Cell 69:559-572 (1992).  
**RN** [3]  
**RP** SEQUENCE OF 14-36.  
**RX** MEDLINE-92208945; PubMed-1348215;  
**RA** Peles E., Bacus S., Koski R.A., Lu H.S., Wen D., Ogden S.G.,  
**RA** Levy R.B., Yarden Y.;  
**RT** "Isolation of the neu/HER-2 stimulatory ligand: a 44 kd glycoprotein  
**RT** that induces differentiation of mammary tumor cells";  
**RL** Cell 69:205-216 (1992).  
**RN** [4]  
**RP** REGULATION OF PROCESSING (ISOFORM ALPHA2C/NDF44).  
**RX** MEDLINE-99069430; PubMed-9852059;  
**RA** Liu X., Hwang H., Cao L., Wen D., Liu N., Graham R.M., Zhou M.;  
**RA** "Release of the neuregulin functional polypeptide requires its  
**RL** cytoplasmic tail";  
**RN** J. Biol. Chem. 273:34335-34340 (1998).  
**RX** INTERACTION WITH LIMK1.  
**RA** MEDLINE-98352096; PubMed-9685409;  
**RA** Wang J.Y., Frenzel K.B., Wen D., Falls D.L.;  
**RT** "transmembrane neuregulins interact with LIM kinase 1, a cytoplasmic  
**RT** protein kinase implicated in development of visuospatial cognition";  
**RL** J. Biol. Chem. 273:20525-20534 (1998).  
**CC** -1- FUNCTION: DIRECT LIGAND FOR ERBB3 AND ERBB4 TYROSINE KINASE  
**CC** RECEPTORS. CONCOMITANTLY RECRUITS ERBB1 AND ERBB2 CORECEPTORS,  
**CC** RESULTING IN LIGAND-STIMULATED TYROSINE PHOSPHORYLATION AND  
**CC** ACTIVATION OF THE ERBB RECEPTORS. THE MULTIPLE ISOFORMS PERFORM  
**CC** DIVERSE FUNCTIONS SUCH AS INDUCING GROWTH AND DIFFERENTIATION OF  
**CC** EPITHELIAL, GLIAL, NEURONAL, AND SKELETAL MUSCLE CELLS; INDUCING  
**CC** EXPRESSION OF ACETYLCHOLINE RECEPTOR IN SYNAPTIC VESICLES DURING  
**CC** THE FORMATION OF THE NEUROMUSCULAR JUNCTION; STIMULATING  
**CC** LOBULOLAMELOLAR BUDGING AND MILK PRODUCTION IN THE MAMMARY GLAND  
**CC** AND INDUCING DIFFERENTIATION OF MAMMARY TUMOR CELLS; STIMULATING  
**CC** SCHWANN CELL PROLIFERATION; IMPLICATION IN THE DEVELOPMENT OF THE  
**CC** MYOCARDIUM SUCH AS TRABECULATION (BY SIMILARITY).  
**CC** -1- SUBUNIT: THE CYTOPLASMIC DOMAIN INTERACTS WITH THE LIM DOMAIN  
**CC** REGION OF LIMK1.  
**-1- SUBCELLULAR LOCATION: EXISTS AS A TYPE I MEMBRANE PROTEIN AND AS A**

**CC** PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE MEMBRANE-  
**CC** BOUND FORM DOES NOT SEEM TO BE ACTIVE.  
**-1- ALTERNATIVE PRODUCTS: AT LEAST 8 ISOFORMS: ALPHA2A/NDF38',  
**CC** ALPHA2B/NDF19, ALPHA2C/NDF44', BETA1, BETA2A/NDF22,  
**CC** BETA3/NDF4 AND BETA4/NDF42A (SHOWN HERE); ARE PRODUCED BY  
**CC** ALTERNATIVE SPlicing.  
**CC** TISSUE SPECIFICITY: WIDELY EXPRESSED. MOST TISSUES CONTAIN ALPHA2A  
**CC** AND ALPHA2B ISOFORMS. ALPHA2 AND BETA2 ARE THE PREDOMINANT FORMS  
**CC** IN MESENCHYMAL AND NONNEURONAL ORGANS. BETA1 IS ENRICHED IN BRAIN  
**CC** AND SPINAL CORD, BUT NOT IN MUSCLE AND HEART. ALPHA2C IS HIGHLY  
**CC** EXPRESSED IN SPINAL CORD, MODERATELY IN LUNG, BRAIN OVARY, AND  
**CC** STOMACH, IN LOW AMOUNTS IN THE KIDNEY, SKIN AND HEART AND NOT  
**CC** DEPICTED IN THE LIVER, SPLEEN, AND PLACENTA.  
**-1- DOMAIN: THE CYTOPASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION OF  
**CC** TRAFFICKING AND PROTEOLYTIC PROCESSING. REGULATION OF THE  
**CC** PROTEOLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN  
**CC** DIMERIZATION.  
**-1- DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE  
**CC** DOMAIN.  
**-1- PTM: PROTEOYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE  
**CC** EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR  
**CC** FORM.  
**-1- PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE.  
**-1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.  
**-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
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**CC** DR EMBL; U02315; AA19940.1.  
**DR** EMBL; U02316; AA19941.1.  
**DR** EMBL; U02317; AA19942.1.  
**DR** EMBL; U02318; AA19943.1.  
**DR** EMBL; U02319; AA19944.1.  
**DR** EMBL; U02320; AA19945.1.  
**DR** EMBL; U02321; AA19946.1.  
**DR** EMBL; U02322; AA19947.1.  
**DR** EMBL; U02316; AA19941.1.  
**DR** EMBL; U02317; AA19942.1.  
**DR** EMBL; U02318; AA19943.1.  
**DR** EMBL; U02319; AA19944.1.  
**DR** EMBL; U02320; AA19945.1.  
**DR** EMBL; U02321; AA19946.1.  
**DR** InterPro; IPR00306; Ig-MIC.  
**DR** InterPro; IPR003598; Ig-c2.  
**DR** InterPro; IPR002154; Neuregulin.  
**DR** Pfam; PF00008; EGF; 1.  
**DR** Pfam; PF00047; Ig; 1.  
**DR** Pfam; PF02158; Neuregulin; 1.  
**DR** PRINTS; PRO1089; NEUREGULIN.  
**DR** SMART; SM0181; EGF; 1.  
**DR** SMART; SM00408; IGC2; 1.  
**DR** PROSITE; PS00022; EGF\_1; 1.  
**DR** PROSITE; PS0186; EGF\_2; FALSE-NEG.  
**DR** Growth factor; EGF-like domain; Immunoglobulin domain; Glycoprotein;  
**DR** KW transmembrane; Multigene family; Alternative splicing.  
**FT** PROPEP 1 13  
**FT** CHAIN 14 662 PRO-NEUREGULIN-1, MEMBRANE-BOUND FORM.  
**FT** CHAIN 14 264 NEUREGULIN-1.  
**FT** DOMAIN 14 265 EXTRACELLULAR (POTENTIAL).  
**FT** DOMAIN 266 288 INTERNAL SIGNAL SEQUENCE (POTENTIAL).  
**FT** DOMAIN 289 662 CYTOPLASMIC (POTENTIAL).  
**FT** DOMAIN 50 119 IG-LIKE C2-TYPE DOMAIN.  
**FT** DOMAIN 165 177 SER/THR-RICH.  
**FT** DOMAIN 178 222 EGF-LIKE.  
**FT** DISULFID 157 112  
**FT** DISULFID 182 196 BY SIMILARITY.  
**FT** DISULFID 190 210 BY SIMILARITY.

FT	DISULFID	212	221	BY SIMILARITY.
FT	CARBOHYD	120	120	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	126	126	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	164	164	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPPLIC	213	256	PNEFTGDRCONVYMASFYWTSRKQOETERPLERLKDHSV KES -> QPFETGACTENPLMKVQOE (IN ISOFORM ALPHA2A, ISOFORM BETA2B AND ISOFORM ALPHA2C).
FT	VARSPPLIC	231	257	MTSRKQOERPLERLKDHSVLSKES -> KHLGIEFME (IN ISOFORM BETA1).
FT	VARSPPLIC	231	241	MTSRKQOETE -> STSPPFPLSE (IN ISOFORM BETA1).
FT	VARSPPLIC	242	662	MISSING (IN ISOFORM BETA2).
FT	VARSPPLIC	231	256	MISSING (IN ISOFORM BETA2 AND ISOFORM BETA2A).
FT	VARSPPLIC	325	330	PPEWQ -> RVRFG (IN ISOFORM BETA2).
FT	VARSPPLIC	446	662	MISSING (IN ISOFORM ALPHA2C).
FT	VARSPPLIC	446	484	YVSANTPAPMSVPTPEHPTSSPKPSEMSPPVSSMTV > HNLIAELRNKNAVRSKCMQIOLSAHLRPSSTHLGFI L (IN ISOFORM ALPHA2B).
FT	VARSPPLIC	485	662	MISSING (IN ISOFORM ALPHA2B).
FT	CONFLICT	90	90	K -> N (IN REF. 2).
FT	CONFLICT	137	137	T -> I (IN REF. 2; AA SEQUENCE).
FT	CONFLICT	208	208	Y -> S (IN REF. 2).
FT	SEQUENCE	662 AA;	73288 MW;	1C31ASCF2A8EB1D5 CRC64;
FT				37.0%; Score 102.5; DB 1; Length 662;
FT				Best Local Similarity 31.2%; Pred. No. 4.9e-05;
FT				Matches 15; Conservative 13; Mismatches 19; Indels 1; Gaps 1;
FT				QY 1 HFPFCRQDGLAYCLNDGCFVFLVLTMSH-CRCKSRYGOSTRCDOFL 47
FT				Db. 178 HJJKCAKKEKTFCVNGGCCFTVKDLNSNPRLCKCPNEFTGDRCONVY 225
	RESULT 9			
	NRGL_CHICK			
FT	NRGL_CHICK	STANDARD;	PRM;	602 AA.
AC	005199; 073750; 073752;			
FT	16-OCT-2001 (Rel. 40, Created)			
FT	16-OCT-2001 (Rel. 40, Last sequence update)			
FT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Pro-neuregulin-1 precursor (Pro-NRGL) [Contains: Neuregulin-1 (Acetylcholine receptor inducing activity) (ARIA)].			
DE	GN OR ARIA.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosuria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OK	NBML_TAXID=9031;			
RN	[1] SEQUENCE FROM N.A. (ISOFORM ARIA), AND PARTIAL SEQUENCE.			
RC	STRAIN=WHITE LEGHORN; TISSUE=Brain;			
RX	Medline-93201602; PubMed-8453670;			
RX	Falls D.L., Rosen K.M., Corfas G., Lane W.S., Fischbach G.D.; "ARIA, a protein that stimulates acetylcholine receptor synthesis, is a member of the neu ligand family.", Cell 72:801-815(1993).			
RT	[2] SEQUENCE FROM N.A. (ISOFORMS BETA1A; BETA2A AND BETA2B).			
RC	SEQUENCE FROM N.A. (ISOFORMS BETA1A; BETA2A AND BETA2B).			
RX	Medline-98150951; PubMed-9491987;			
RX	Yang X., Kuo J., Devay P., Yu C.; Role 1.; "A cysteine-rich isoform of neuregulin controls the level of expression of neuronal nicotinic receptor channels during synaptogenesis"; Neuron 20:255-270(1998).			
RT	1- FUNCTION: DIRECT LIGAND FOR THE ERBB TYROSINE KINASE RECEPTORS.			
CC	THE MULTIPLE ISOFORMS PERFORM DIVERSE FUNCTIONS: CSTEIN-RICH DOMAIN CONTAINING ISOFORMS (CRD-NRG) PROBABLY REGULATE THE EXPRESSION OF NICOTINIC ACETYLCHOLINE RECEPTORS AT DEVELOPING INTERNEURONAL SYNAPSES. THE IG-NGR ISOFORM IS REQUIRED FOR THE INITIAL INDUCTION AND/OR MAINTENANCE OF THE MATURE LEVELS OF			
CC	ACETYLCHOLINE RECEPTORS AT NEUROSCULAR SYNAPSES.			
CC	-1-- SUBCELLULAR LOCATION: EXISTS AS A TYPE-I MEMBRANE PROTEIN AND AS A PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE MEMBRANE- BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).			
CC	-1- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS (ARIA/IG-NRG (SHOWN HERE), CRD-NRG-BETA1A, CRD-NRG-BETA2A AND CRD-NRG-BETA2B; ARE PRODUCED BY ALTERNATIVE SPLICING. ARIA CONTAINS AN IG-LIKE DOMAIN REPLACED BY A CYSTEINE-RICH DOMAIN (CRD).			
CC	-1-- DEVELOPMENTAL STAGE: CRD-ARING ISOFORM IS DETECTED AT EMBRYONIC DAY 4 (ED4) IN BOTH VISCERAL AND SOMATIC MOTOR NEURONS OF SPINAL CORD AND IS HIGHEST AT ED6. IG-NRG ISOFORM IS NOT EXPRESSED UNTIL ED6 IN SPINAL CORD. AT ED 11 BOTH ISOFORMS DISPLAY COMPARABLE LEVELS.			
CC	-1- DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION OF TRAFFICKING AND PROTEOLYTIC PROCESSING. REGULATION OF THE PROTEOLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN DIMERIZATION (BY SIMILARITY).			
CC	-1- DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE DOMAIN.			
CC	-1- PTM: PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR FORM.			
CC	-1- PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE (BY SIMILARITY).			
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN LIKE C2-TYPE DOMAIN.			
CC	-1- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.			
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CC	DR	EMBL: L11264; AAA49037; -		
DR	EMBL: AAF495654; AAC05670; -			
DR	EMBL: AF045655; AAC05671; -			
DR	EMBL: AF045656; AAC05672; -			
DR	HSSP: Q12784; IHR:			
DR	InterPro: IPR000561; EGFLike:			
DR	InterPro: IPR003006; Ig_MHC:			
DR	InterPro: IPR03598; Ig_C2:			
DR	InterPro: IPR02114; Neuregulin.			
DR	Pfam: PF00047; 19; 1.			
DR	Pfam: PF02158; Neuregulin; 1.			
DR	PRINTS: PR01089; NEUREGULIN.			
DR	SMART: SNO0181; EGF; 1.			
DR	SMART: SNO0408; IgC2; 1.			
DR	PROSITE: PS00022; EGF_1; 1.			
DR	PROSITE: PS01186; EGF_2; FALSE_NEG.			
DR	Transmembrane; Alternative splicing.			
KW	Transmembrane; Immunoglobulin domain; Glycoprotein;			
FT	CHAIN 1 602 PRO-NEUREGULIN-1, MEMBRANE-BOUND FORM.			
FT	DOMAIN 1 205 NEUREGULIN-1.			
FT	DOMAIN 1 206 EXTRACELLULAR (POTENTIAL).			
FT	TRANSMEM 207 229 INTERNAL SIGNAL SEQUENCE (POTENTIAL).			
FT	DOMAIN 230 602 CYTOPLASMIC (POTENTIAL).			
FT	DOMAIN 42 112 IG-LIKE C2-TYPE DOMAIN.			
FT	DOMAIN 125 136 SER/THR RICH.			
FT	DOMAIN 137 181 EGF-LIKE.			
FT	DISULFID 49 105 BY SIMILARITY.			
FT	DISULFID 141 155 BY SIMILARITY.			
FT	DISULFID 149 169 BY SIMILARITY.			
FT	DISULFID 171 180 BY SIMILARITY.			
FT	CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	VARSPPLIC 1 1 MWSSEGQLQLSLAPLQPTDUNVSYNTTPVKRKKPENQEV GQKVLVRCETTETPALKPKWVQKNGKQEV			
FT	KKRYKSEYLRTADLAGEYVACRVSQKLGNSDKSVAIT DPA -> MWSSEGQLQLSLAPLQPTDUNVSYNTTPVKRKKPENQEV			

NCB2_HUMAN	191	198	PRR;	850 AA.
ID	NRG2_HUMAN	STANDARD;		
AC	Q14511;			
DT	15-DEC-1998	(Rel. 37, Created)		
DT	16-DEC-1998	(Rel. 37, Last sequence update)		
DE	Pro-neuregulin-2 precursor (Pro-NRG2) [Contains: Neuregulin-2 (NRG-2) (Neural and thymus-derived activator for ERBB Kinases) (NRK) (Divergent of neuregulin 1) (DON-1)].			
DE	NRG2 OR NTK.			
OS	Homo sapiens (Human).			
OC	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; OX			
RN	NBLX_Taxid:9606;			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Neuroblastoma;			
RA	MEDLINE=98006324; PubMed=94848101;			
RA	Higashiyama S., Horikawa M., Yamada K., Ichino N., Nakano N., Nakaya T., Miyagawa J., Matsushita N., Nagatsu T., Taniguchi N., Ishiguro H.: "A novel brain-derived member of the epidermal growth factor family that interacts with Erbb3 and Erbb4."; J. Biochem. 122:675-680(1997).			
RL	[2]			
RN	SEQUENCE FROM N.A. (ISOFORMS DON-1B AND DON-1R).			
RC	TISSUE=fetal brain;			
RA	MEDLINE=97342638; PubMed=9199335;			
RA	Busfield S.J., Michnick D.A., Chickering T.W., Revett T.L., Ma J., Woolf E.A., Comack C.A., Dussault B.J., Woolf J., Goodearl A.D.J., Gearling D.P.;			
RT	"Characterization of a neuregulin-related gene, Don-1, that is highly expressed in restricted regions of the cerebellum and hippocampus."; Mol. Cell. Biol. 17:4007-4014(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6).			
RC	TISSUE=Lung, and Fetal brain;			
RA	MEDLINE=99395836; PubMed=369162;			
RL	"Ring H.2., Chang H., Guillet A., Brice A., LeGuenn E., Francke U.; resulting in ligand-stimulated tyrosine phosphorylation and activation of the Erbb receptors. May also promote the heterodimerization with the EGF receptor.";			
RL	Hum. Genet. 104:326-359 (1999).			
CC	- FUNCTION: DIRECT LIGAND FOR ERBB3 AND ERBB4 TYROSINE KINASE RECEPTORS. CONCOMITANTLY RECRUTS ERBB1 AND ERBB2 CORECEPTORS, AS A CANDIDATE FOR THE AUTOSOMAL RECESSIVE FORM OF CHARCOT-MARIE-TOOTH DISEASE LINKED TO 5q.;			
CC	"- HETERO-DIMERIZATION WITH THE EGF RECEPTOR. MAY ALSO PROMOTE THE HETERO-DIMERIZATION WITH THE EGF RECEPTOR.";			
CC	"- FUNCTION: EXISTS AS AN TYPE I MEMBRANE PROTEIN AND AS A PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE			

MEMBRANE-BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).

-1 - ALTERNATIVE PRODUCTS: 8 ISOMERS; 1 (SHOWN HERE), 2, 3, 4, 5, 6, DON-1B AND DON-1R; ARE PRODUCED BY ALTERNATIVE SPlicing.

-1 - TISSUE SPECIFICITY: RESTRICTED TO THE CEREBELLUM IN THE ADULT.

-1 - DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION OF TRAFFICKING AND PROTEOLYTIC PROCESSING. REGULATION OF THE PROTEOLYTIC PROCESSING INVOLVES THE INITIAL INTRACELLULAR DOMAIN DIMERIZATION (BY SIMILARITY).

-1 - DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE DOMAIN (BY SIMILARITY).

-1 - PTM: PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR FORM (BY SIMILARITY).

-1 - PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE (BY SIMILARITY).

-1 - SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

-1 - SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

-1 - SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.

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		Best Local Similarity		Pred. No.		Indels		Gaps	
		Matches		15; Conservative		9; Mismatches		17;	
DR	EMBL: AF119153; AF28852; 1; JOINED.								
DR	EMBL: AF119154; AF28852; 1; JOINED.								
DR	EMBL: AF119155; AF28852; 1; JOINED.								
DR	EMBL: AF119156; AF28852; 1; JOINED.								
DR	EMBL: AF119157; AF28853; 1; JOINED.								
DR	EMBL: AF119151; AF28853; 1; JOINED.								
DR	EMBL: AF119153; AF28853; 1; JOINED.								
DR	EMBL: AF119154; AF28853; 1; JOINED.								
DR	EMBL: AF119156; AF28853; 1; JOINED.								
DR	HSSP: Q12784; IIRE.								
DR	InterPro: IPR00561; EGF-1.								
DR	InterPro: IPR003006; Ig_MHC.								
DR	InterPro: IPR03598; Ig_C2.								
DR	InterPro: IPR02154; Neuregulin.								
DR	Pfam: PF00008; EGF.								
DR	Pfam: PF0047; Ig_1.								
DR	Pfam: PF02158; Neuregulin.								
DR	SMART: SM00101; SCP.								
DR	SMART: SM00408; IgC2.								
DR	ROSITE: S00022; EGF_1.								
DR	PROSITE: PS01186; EGF_2.								
DR	KW	Transmembrane; Multigene family; Immunoglobulin domain; Glycoprotein;							
DR	KW	Transmembrane; Multigene family; Alternative splicing.							
FT	PROTEIN	1	111	BY SIMILARITY.					
FT	CHAIN	112	850	PRO-NEUREGULIN-2, MEMBRANE-BOUND FORM.					
FT	CHAIN	112	404	NEUREGULIN-2.					
FT	DOMAIN	112	405	EXTRACELLULAR (POTENTIAL).					
FT	TRANSMEM	406	426	INTERNAL SIGNAL SEQUENCE (POTENTIAL).					
FT	DOMAIN	427	850	CYTOPLASMIC (POTENTIAL).					
FT	DOMAIN	318	318	IG-LIKE C2-TYPE DOMAIN.					
FT	DOMAIN	330	382	SER/THR-RICH.					
FT	DOMAIN	341	13	EGF-LIKE.					
FT	DOMAIN	10	30	POLY-PRO.					
FT	DOMAIN	33	47	POLY-SER.					
FT	DOMAIN	87	90	POLY-ALA.					
FT	DOMAIN	721	727	POLY-PRO.					
FT	DISULFID	257	311	BY SIMILARITY.					
FT	DISULFID	345	359	BY SIMILARITY.					
FT	DISULFID	353	370	BY SIMILARITY.					
FT	DISULFID	372	381	BY SIMILARITY.					
FT	CARBODY	52	52	N-LINKED (GLCNAC. ) (POTENTIAL).					
FT	CARBODY	53	53	N-LINKED (GLCNAC. ) (POTENTIAL).					
FT	CARBODY	147	147	N-LINKED (GLCNAC. ) (POTENTIAL).					
FT	CARBODY	278	278	N-LINKED (GLCNAC. ) (POTENTIAL).					
FT	CARBODY	346	346	N-LINKED (GLCNAC. ) (POTENTIAL).					
FT	VARSPLIC	1	233	MOVCCSALPPPLEGKGSYDSSSSERESSSSSSSS					
FT	VARSPLIC	1	241	ESGSRSNSNSISRPAPKPEPKQDQPRPAAKAA					
FT	VARSPLIC	1	396	ARSRAAAGGMRDAPGSPMMGLGVSLACPSPLSKVQD					
FT	VARSPLIC	1	397	AKAPVYVEGKGQVGLYPAGGSSNSTRPAPGAVLWL					
FT	VARSPLIC	1	397	DKHLRLSSGQKQEVIVSGCVPJLERNQYFLEFTEPQL					
FT	VARSPLIC	1	397	VFKVAFAPLDTNGKMKKEVKGKILCTDC -> MESSRKG					
FT	VARSPLIC	1	397	GRRGKHPGKRRKRRERPDGK (IN ISOFORM DON-1).					
FT	VARSPLIC	1	397	MISSING (IN ISOFORM DON-1B).					
FT	VARSPLIC	1	397	NGFGQRGQLEKPLRQYHDPKQ -> VGYTGRQOFAMV					
FT	VARSPLIC	1	397	NFS (IN ISOFORM 2).					
FT	VARSPLIC	1	397	KARELYQYRVLTTGICVALLYVGIV -> SVLMDTPGIV					
FT	VARSPLIC	1	397	SQSSSTPSRVDLQIN (IN ISOFORM 6).					
FT	VARSPLIC	1	397	MISSING (IN ISOFORM 6).					
FT	VARSPLIC	1	426	KARELYQYRVLTTGICVALLYVGIVCA -> SVLMDTP					
FT	VARSPLIC	1	426	CGVSSSOMSKPNSPRTRRS (IN ISOFORM 5).					
FT	SEQUENCE	850	850	MISSING (IN ISOFORM 5).					
FT	SEQUENCE	850	850	91678 MW; 7124C089435FD2F4 CRC64;					
Query Match		32.5%	Score 90;	DB 1;	Length 850;				

RESULT. 11

NRG2\_RAT

ID NRG2\_RAT

AC 035569; 035570; 035571; 035073;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pro-neuregulin-2 precursor (Pro-NRG2) (Contains: Neuregulin-2 (NRG-2))

DE (Neural and thymus-derived activator for ERBB kinases) (NTAK).

GN NRG2 OR NTAK.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Rattus.

OX NCBI\_TAXID=10116;

RN [1]

RP SEQUENCE FROM N.A. SEQUENCE OF 128-162, AND ALTERNATIVE SPlicing.

RA MEDLINE-98006324; PubMed-936101;

RA Hiyashiyama S., Horikawa M., Yamada K., Ichino N., Nakano N., Nakagawa T., Miyagawa J., Matsushita N., Nagatsu T., Taniguchi N., Ishiguro H.

RA "A novel brain-derived member of the epidermal growth factor family that interacts with ErbB3 and ErbB4,"

RA Chang H., Riese D. J. II, Gilbert W., Stern D.-F., McMahon U.-J.; RT "Ligands for ErbB-family receptors encoded by a neuregulin-like gene,"

RA Nature, 387:509-512(1997).

CC -1- FUNCTION: DIRECT LIGAND FOR ERBB3 AND ERBB4 TYROSINE KINASE RECEPTORS. CONCOMITANTLY RECRUITS ERBB1 AND ERBB2 CORECEPTORS, RESULTING IN LIGAND-STIMULATED TYROSINE PHOSPHORYLATION AND ACTIVATION OF THE ERBB RECEPTORS. MAY ALSO PROMOTE THE HETEROODIMERIZATION WITH THE EGF RECEPTOR.

CC -1- SUBCELLULAR LOCATION: EXISTS AS AN TYPE I MEMBRANE PROTEIN AND AS A PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE MEMBRANE-BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).

CC -1- ALTERNATIVE PRODUCTS: AT LEAST 7 ISOFORMS: NTAK-ALPHAL (SHOWN HERE), NTAK-ALPHA2A, NTAK-ALPHA2B, NTAK-ALPHA2B, NTAK-ALPHA2B, GAMMA, NRG2-ALPHA AND NRG2-BETA; ARE PRODUCED BY ALTERNATIVE SPlicing. THE ALPHA-TYPE AND BETA-TYPE DIFFER IN THE EGF-LIKE DOMAIN.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOST PARTS OF THE BRAIN, ESPECIALLY THE OLFACTORY BULB AND CEREBELLUM WHERE IT LOCALIZES IN GRANULE CELLS OF THE DENTATE GYRUS. IN THE HIPPOCAMPUS, FOUND IN THE CHOLINERGIC CELLS. IN THE HINDBRAIN, WEAKLY DETECTABLE IN THE MOTOR CEREBRAL NUCLEUS. NOT DETECTED IN THE HYPOTHALAMUS, ALSO FOUND IN THE LIVER AND IN THE THYMUS. NOT DETECTED IN HEART, ADRENAL GLAND, OR TESTIS.

CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, EXPRESSED IN THE BRAIN OF E11.5 EMBRYOS WHERE IT IS FOUND IN THE TELENCEPHALON, BUT NOT IN THE HINDBRAIN. NOT FOUND IN THE HEART. IN THE ADULT, FOUND IN BRAIN AND THYMUS.

CC -1- DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION OF TRAFFICKING AND PROTEOLYTIC PROCESSING. REGULATION OF THE PROTEOLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DIMERIZATION (BY SIMILARITY).

CC -1- DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE DOMAIN (BY SIMILARITY).

CC -1- PTM: PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR (BY SIMILARITY).

		Query Match	Score	DB	Length
CC	-1 PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE (BY SIMILARITY).	32.5%	90	DB 1;	868;
CC	-1 SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.	Best Local Similarity	34.9%	Pred. No.	0.002;
CC	-1 SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.	Matches	15;	Conservative	9;
CC	-1 SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.	Mismatches	17;	Indels	2;
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).				
CC	-----				
CC	DR EMBL: D89995; BAA23344.1;	RESULT 12			
CC	DR EMBL: D89996; BAA23345.1;	ID EREG_HUMAN			
CC	DR EMBL: D89997; BAA23346.1;	STANDARD:			
CC	DR EMBL: D89998; BAA23347.1;	PRT:	169 AA.		
CC	DR EMBL: AB00176; BAA23348.1;	AC 014944;			
CC	DR EMBL: 012784; IHRB.	DT 30-MAY-2000 (Rel. 39, Created)			
CC	DR InterPro: IPR000561; EGF-like.	DT 30-MAY-2000 (Rel. 39, Last sequence update)			
CC	DR InterPro: IPR003061; Ig_MRC.	DT 16-OCT-2001 (Rel. 40, Last annotation update)			
CC	DR InterPro: IPR003598; Ig_C2.	DE Epiregulin Precursor.			
CC	DR InterPro: IPR002154; Neuregulin.	GN EREG.			
CC	DR Pfam: PP00008; EGF_1.	RC Homo sapiens (Human)			
CC	DR Pfam: PP00047; Ig_1.	RA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	DR Pfam: PP02158; Neuregulin; 2.	OC Mammalia; Eutheria; Primates; Catarrhini; Homino.			
CC	DR SMART: SM00181; EGF_1.	OX NCBI_TaxID:9605;			
CC	DR SMART; SM00408; IgG2_1.	RN [1]			
CC	DR PROSITE: PS0022; EGF_1; 1.	RP SEQUENCE FROM N.A., AND CHARACTERIZATION.			
CC	DR PROSITE: PS01186; EGF_2; 1.	TISSUE=Colorectal adenocarcinoma;			
CC	DR PROSITE: PS01186; EGF_2; 1.	RX MEDLINE=9749200; PubMed=9337852;			
CC	DR PROSITE: PS01186; EGF_2; 1.	RA Toyoda H., Komurasaki T., Uchida D., Morimoto S.;			
CC	DR PROSITE: PS01186; EGF_2; 1.	RT "Distribution of mRNA for human epiregulin, a differentially expressed member of the epidermal growth factor family.";			
CC	DR PROSITE: PS01186; EGF_2; 1.	RL Biochem. J. 326:69-75 (1997).			
CC	DR PROSITE: PS01186; EGF_2; 1.	CC -1- FUNCTION: MAY BE A MEDiator OF LOCALIZED CELL PROLIFERATION AS A MITOGEN IT MAY STIMULATE CELL PROLIFERATION AND/OR ANGIOGENESIS.			
CC	DR PROSITE: PS01186; EGF_2; 1.	CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (PRECURSOR FORM); EXTRACELLULAR (MATURE FORM).			
CC	DR PROSITE: PS01186; EGF_2; 1.	CC -1- TISSUE SPECIFICITY: IN NORMAL ADULTS EXPRESSED PREDOMINANTLY IN THE PLACENTA AND PERIPHERAL BLOOD LEUCOCITES. HIGH LEVELS WERE DETECTED IN CARCINOMAS OF THE BLADDER, LUNG, KIDNEY AND COLON.			
CC	DR PROSITE: PS01186; EGF_2; 1.	CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.			
CC	DR DISULFID 361; 375; BY SIMILARITY.	DR -----			
CC	DR DISULFID 369; 397; BY SIMILARITY.	DR -----			
CC	DR DISULFID 388; 397; BY SIMILARITY.	DR -----			
CC	DR CARBOHYD 33; 33; N-LINKED (GLCNAC. . .) (POTENTIAL).	DR -----			
CC	DR CARBOHYD 34; 34; N-LINKED (GLCNAC. . .) (POTENTIAL).	DR -----			
CC	DR CARBOHYD 163; 163; N-LINKED (GLCNAC. . .) (POTENTIAL).	DR -----			
CC	DR CARBOHYD 294; 294; N-LINKED (GLCNAC. . .) (POTENTIAL).	DR -----			
CC	DR CARBOHYD 362; 362; N-LINKED (GLCNAC. . .) (POTENTIAL).	DR -----			
CC	DR VARSPLIC 1; 108; MISSING (IN ISOFORM NRG2-BETA).	DR -----			
CC	DR VARSPLIC 220; 222; PLY-> PFF (IN ISOFORM NRG2-BETA-1P).	DR -----			
CC	DR VARSPLIC 388; 388; C -> G (IN ISOFORM NTRK-ALPHA2-1P).	DR -----			
CC	DR VARSPLIC 389; 868; MISSING (IN ISOFORM NTRK-GAMMA).	DR -----			
CC	DR VARSPLIC 412; 412; NQFFGQCLERPLRQYMPDKQ -> VGYTGDRQOFAMV	DR -----			
CC	DR VARSPLIC 390; 421; NQFFGQCLERPLRQYMPDKQHGFELKE -> VGYTGDRQOFAMV	DR -----			
CC	DR VARSPLIC 414; 421; DQCGQPAWNSK (IN ISOFORM NTRK-BETA).	DR -----			
CC	DR VARSPLIC 390; 421; MISSING (IN ISOFORM NTRK-ALPHA2 AND ISOFORM NTRK-ALPHA2B).	DR -----			
CC	DR VARSPLIC 414; 439; HLGFLKREAEELPLRQYMPDKQ -> VGYTGDRQOFAMV	DR -----			
CC	DR VARSPLIC 440; 868; SSSQWSTPSPLDLYN (IN ISOFORM NRG2-ALPHA).	DR -----			
CC	DR VARSPLIC 117; 117; MISSING (IN ISOFORM NRG2-ALPHA).	DR -----			
CC	DR VARSPLIC 724; 724; R -> H (IN REF. 2).	DR -----			
CC	DR VARSPLIC 868 AA; 93776 MW; 3C7D4D9DBE6DE2 CRC64;	DR -----			
SO	Query Match	32.5%	Score	90;	DB 1;
SO	Best Local Similarity	40.5%	Length	169;	Pred. No. 0.0005;



FT	DOMAIN	178	216	EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	456	467	BY SIMILARITY.
FT	DOMAIN	218	255	EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	461	476	BY SIMILARITY.
FT	DOMAIN	257	293	EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	478	487	BY SIMILARITY.
FT	DOMAIN	295	333	EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	494	505	BY SIMILARITY.
FT	DOMAIN	335	371	EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	499	514	BY SIMILARITY.
FT	DOMAIN	372	410	EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	515	525	BY SIMILARITY.
FT	DOMAIN	412	450	EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	532	543	BY SIMILARITY.
FT	DOMAIN	452	488	EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	537	552	BY SIMILARITY.
FT	DOMAIN	490	526	EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	554	563	BY SIMILARITY.
FT	DOMAIN	528	564	EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	570	580	BY SIMILARITY.
FT	DOMAIN	566	601	EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	575	589	BY SIMILARITY.
FT	DOMAIN	603	639	EGF-LIKE 16, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	591	600	BY SIMILARITY.
FT	DOMAIN	641	676	EGF-LIKE 17, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	607	618	BY SIMILARITY.
FT	DOMAIN	678	714	EGF-LIKE 18, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	612	627	BY SIMILARITY.
FT	DOMAIN	716	751	EGF-LIKE 19, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	629	638	BY SIMILARITY.
FT	DOMAIN	753	789	EGF-LIKE 20, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	645	655	BY SIMILARITY.
FT	DOMAIN	791	827	EGF-LIKE 21, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	650	664	BY SIMILARITY.
FT	DOMAIN	829	867	EGF-LIKE 22, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	666	675	BY SIMILARITY.
FT	DOMAIN	869	905	EGF-LIKE 23, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	682	693	BY SIMILARITY.
FT	DOMAIN	907	943	EGF-LIKE 24, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	687	702	BY SIMILARITY.
FT	DOMAIN	945	981	EGF-LIKE 25, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	704	713	BY SIMILARITY.
FT	DOMAIN	983	1019	EGF-LIKE 26.	FT	DISULFID	720	730	BY SIMILARITY.
FT	DOMAIN	1021	1057	EGF-LIKE 27, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	725	739	BY SIMILARITY.
FT	DOMAIN	1059	1095	EGF-LIKE 28.	FT	DISULFID	741	750	BY SIMILARITY.
FT	DOMAIN	1097	1143	EGF-LIKE 29.	FT	DISULFID	757	768	BY SIMILARITY.
FT	DOMAIN	1145	1181	EGF-LIKE 30, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	762	777	BY SIMILARITY.
FT	DOMAIN	1183	1219	EGF-LIKE 31, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	779	788	BY SIMILARITY.
FT	DOMAIN	1221	1265	EGF-LIKE 32, CALCIUM-BINDING (POTENTIAL).	FT	DISULFID	795	806	BY SIMILARITY.
FT	DOMAIN	1267	1305	EGF-LIKE 33.	FT	DISULFID	800	815	BY SIMILARITY.
FT	DOMAIN	1307	1348	EGF-LIKE 34.	FT	DISULFID	817	826	BY SIMILARITY.
FT	DOMAIN	1348	1384	EGF-LIKE 35.	FT	DISULFID	833	844	BY SIMILARITY.
FT	DOMAIN	1387	1426	EGF-LIKE 36.	FT	DISULFID	838	855	BY SIMILARITY.
FT	DOMAIN	1449	1480	CYS-RICH.	FT	DISULFID	857	866	BY SIMILARITY.
FT	REPEAT	1445	1480	LIN/NOTCH 1.	FT	DISULFID	873	884	BY SIMILARITY.
FT	REPEAT	1481	1522	LIN/NOTCH 2.	FT	DISULFID	878	893	BY SIMILARITY.
FT	REPEAT	1523	1562	LIN/NOTCH 3.	FT	DISULFID	895	904	BY SIMILARITY.
FT	REPEAT	1917	1947	ANK 1.	FT	DISULFID	911	922	BY SIMILARITY.
FT	REPEAT	1949	1979	ANK 2.	FT	DISULFID	916	931	BY SIMILARITY.
FT	REPEAT	1983	2012	ANK 3.	FT	DISULFID	933	942	BY SIMILARITY.
FT	REPEAT	2045	2049	ANK 4.	FT	DISULFID	947	948	BY SIMILARITY.
FT	REPEAT	2049	2048	ANK 5.	FT	DISULFID	992	1007	BY SIMILARITY.
FT	DISULFID	24	37	BY SIMILARITY.	FT	DISULFID	1009	1018	BY SIMILARITY.
FT	DISULFID	31	46	BY SIMILARITY.	FT	DISULFID	1025	1036	BY SIMILARITY.
FT	DISULFID	63	74	BY SIMILARITY.	FT	DISULFID	1036	1045	BY SIMILARITY.
FT	DISULFID	68	87	BY SIMILARITY.	FT	DISULFID	1047	1056	BY SIMILARITY.
FT	DISULFID	89	98	BY SIMILARITY.	FT	DISULFID	1047	1056	BY SIMILARITY.
FT	DISULFID	106	117	BY SIMILARITY.	FT	DISULFID	1063	1074	BY SIMILARITY.
FT	DISULFID	111	127	BY SIMILARITY.	FT	DISULFID	1063	1074	BY SIMILARITY.
FT	DISULFID	129	138	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.
FT	DISULFID	144	155	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.
FT	DISULFID	149	164	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.
FT	DISULFID	166	175	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.
FT	DISULFID	182	195	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.
FT	DISULFID	189	204	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.
FT	DISULFID	206	215	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.
FT	DISULFID	222	227	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.
FT	DISULFID	227	243	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.
FT	DISULFID	245	254	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.
FT	DISULFID	261	272	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.
FT	DISULFID	266	281	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.
FT	DISULFID	283	292	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.
FT	DISULFID	306	321	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.
FT	DISULFID	323	332	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.
FT	DISULFID	339	350	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.
FT	DISULFID	344	359	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.
FT	DISULFID	361	370	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.
FT	DISULFID	376	387	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.
FT	DISULFID	381	398	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.
FT	DISULFID	400	409	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.
FT	DISULFID	416	429	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.
FT	DISULFID	423	438	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.
FT	DISULFID	449	449	BY SIMILARITY.	FT	DISULFID	1074	1074	BY SIMILARITY.

Query Match Score: 30.0%; DB: 1; Length: 2531;  
 Best Local Similarity: 41.7%; Pred. No.: 0.07%;  
 Matches: 15; Conservative: 4; Mismatches: 13; Indels: 4; Gaps: 1;

QY 9 DAYCLNDGECCVFIELTQLGSHKHCRCKEQYGRCD 44  
 Db 1064 DSACKNSGRCW---QINTQHNCERCSWQNG 1095

RESULT 15  
 BTC\_MOUSE  
 ID BTC\_MOUSE STANDARD: PRT: 177 AA.  
 AC 005928;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Beta-cellulin precursor (BTC).  
 GN BTC OR BCN.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NCBI\_TAXID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 32-54; 64-71 AND 75-111.  
 RX MEDLINE=93206093; PubMed=8456283;

RA	Shing Y., Christoforaki G., Hanahan D., Ono Y., Sasada R.,
RT	"Betacellulin, a mitogen from pancreatic beta cell tumors.",
RL	Science 259:1604-1607 (1993).
CC	-1- FUNCTION: POTENT MITOGEN FOR RETINAL PIGMENT EPITHELIAL CELLS
CC	AND VASCULAR SMOOTH MUSCLE CELLS. THE EFFECTS OF BETACELLULIN
CC	ARE PROBABLY MEDIATED BY THE EGF RECEPTOR AND OTHER RELATED
CC	RECEPTORS.
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (PRECURSOR FORM);
CC	EXTRACELLULAR (MATURE FORM).
CC	-1- TISSUE SPECIFICITY: FOUND IN SEVERAL MOUSE TISSUES INCLUDING
CC	KIDNEY, UTERUS AND LIVER AS WELL AS IN BETA TUMOR CELL LINE AND
CC	MCF-7 CELLS. IT IS NOT DETECTED IN THE BRAIN.
CC	-1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> )
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
DR	EMBL: L08394; AAA40511.1;
DR	PIR: A37408; A37408.
DR	HSSP: P01135; JIGF.
DR	MGD: MGI:99439; Btc.
DR	InterPro: IPR00561; EGF-like.
DR	InterPro: IPR01336; EGF_1.
DR	Pfam: PF00008; EGF_1.
DR	PRINTS: PR00009; EGFGP.
DR	SMART: SM00181; EGF_1.
DR	PROSITE: PS00022; EGF_1.
DR	PROSITE: PS0116; EGF_2.
KW	Growth factor; Mitogen; Glycoprotein; EGF-like domain; Transmembrane;
KW	Signal.
FT	1 31
FT	CHAIN 32 111
FT	PROPER 112 177
FT	DOMAIN 32 118
FT	TRANSMEM 119 139
FT	140 177
FT	65 105
FT	146 153
FT	69 82
FT	77 93
FT	95 104
FT	34 34
FT	42 42
FT	52 52
SQ	SEQUENCE 177 AA; 19564 MW; 066B34F0B13F02B C064;
Query	Match
Best Local Similarity	29.8%
Matches	18;
Conservative	9;
Mismatches	14;
Indels	5;
Gaps	3;

GenCore version 5.1.3 Copyright (c) 1993 - 2002 CompuGen Ltd.													
OM protein - protein search, using sw model													
Run on: November 7, 2002, 09:59:08 ; Search time 19 Seconds													
(without alignments)													
237.695 Million cell updates/sec													
<b>Title:</b>	<b>US-09-480-977-4</b>	<b>Post-processing:</b>	<b>BL0SUM62</b>	<b>Scoring table:</b>	<b>Gapop 10.0 , Gapext 0.5</b>	<b>Searched:</b>	<b>283138 seqs, 96089334 residues</b>	<b>total number of hits satisfying chosen parameters:</b>	<b>283138</b>				
Minimum DB seq length: 0													
Maximum DB seq length: 200000000													
Maximum Match 0%													
Listing first 45 summaries													
<b>database :</b>	<b>PRR_71:*</b>	<b>1:</b>	<b>PR1:*</b>	<b>2:</b>	<b>PR2:*</b>	<b>3:</b>	<b>PR3:*</b>	<b>4:</b>	<b>PR4:*</b>				
pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.													
SUMMARIES													
<b>Result No.</b>	<b>Score</b>	<b>Query Match</b>	<b>Length</b>	<b>DB ID</b>	<b>Description</b>								
1	277	100.0	713	2	T4447								
2	113.5	41.0	125	2	I33405	neuregulin-3 [imported] - mouse							
3	113.5	41.0	462	2	I38404	C;Species: <b>Mus musculus</b> (house mouse)							
4	113.5	41.0	640	2	A43273	C;Accession: T4447							
5	111.5	40.3	639	2	I61719	R;Zhang, D.; Sliwkowski, M.X.; Mark, M.; Frantz, G.; Alita, R.; Sun, Y.; Hillan, K.							
6	105.5	38.1	125	2	S62670	Proc. Natl. Acad. Sci. U.S.A. 94, 9562-9567, 1997							
7	105.5	37.7	2			A;Title: Neuregulin-3 (NRG3) - A novel tissue-enriched protein that binds and							
8	104.5	37.7	241	2	S32359	A;Reference number: 222773; NID:97420720							
9	104.5	37.7	241	2	D43273	A;Accession: T4447							
10	104.5	37.7	296	2	S32357	A;Status: preliminary; translated from GB/EMBL/DBJ							
11	104.5	37.7	422	2	S32357	A;Molecule type: mRNA							
12	104.5	37.7	637	2	C43273	A;Residues: 1-113 <2HA>							
13	104.5	37.7	645	2	B43273	A;Cross-references: EMBL:AF010130; NID:92429163; PID:AB70914.1; PID:92429164							
14	102.5	37.0	230	2	A56210	C;Genetics: C;Gene: NRG3							
15	102.5	37.0	636	2	I61718	Query Match 100.0%; Score 277; DB 2; Length 713;							
16	102.5	37.0	662	2	I61722	Best Local Similarity 100.0%; Pred. No. 4.7e-24; Mismatches 0; Indels 0; Gaps 0;							
17	98.5	602	2		A45760	Matches 47; Conservative							
18	92.5	33.4	2180	2	T29764	RESULT 2							
19	90	32.5	90	2	JCS702	Query Match 100.0%; Score 277; DB 2; Length 713;							
20	90	32.5	860	2	JCS701	C;Species: Homo sapiens (man)							
21	90	32.5	868	2		C;Accession: T4447							
22	85	30.7	1		EGVZT	C;Date: 28-May-1998 #sequence_revision 29-May-1998 #text_change 05-Nov-1999							
23	84.5	30.5	1220	2	A56135	C;Accession: T4447							
24	83	30.0	46	2	JT0747	R;Wen, D.; Suggs, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, T.; Mol. Cell. Biol. 14, 1909-1919, 1994							
25	83	30.0	162	2	S68401	A;Title: structural and functional aspects of the multiplicity of Neu differentiation							
26	83	30.0	861	2	A48825	A;Reference number: A56210; NID:9158863							
27	83	30.0	2531	2	A46019	A;Accession: T44405							
28	82.5	29.8	177	2	A37408	A;Status: preliminary; translated from GB/EMBL/DDJB							
29	82	29.6	85	1	EGVZMA	A;Molecule type: mRNA							
A;Residues: 1-125 <RHS>													
A;Cross-references: EMBL:002327; NID:9408404; PIDN:AAA1952.1; PID:9408405													
Query Match 41.0%; Score 113.5; DB 2; Length 125;													
Best Local Similarity 34.8%; Pred. No. 5.1e-06; Mismatches 15; Indels 1; Gaps 1;													
Matches 16; Conservative 14; Mismatches 15; Indels 1; Gaps 1;													
ALIGNMENTS													
RESULT 1													
T4447													
neuregulin-3 [imported] - mouse													
C;Species: <b>Mus musculus</b> (house mouse)													
C;Accession: T4447													
R;Zhang, D.; Sliwkowski, M.X.; Mark, M.; Frantz, G.; Alita, R.; Sun, Y.; Hillan, K.													
Proc. Natl. Acad. Sci. U.S.A. 94, 9562-9567, 1997													
A;Title: Neuregulin-3 (NRG3) - A novel tissue-enriched protein that binds and													
A;Reference number: 222773; NID:97420720													
A;Accession: T4447													
A;Status: preliminary; translated from GB/EMBL/DBJ													
A;Molecule type: mRNA													
A;Residues: 1-113 <2HA>													
C;Cross-references: EMBL:AF010130; NID:92429163; PIDN:AB70914.1; PID:92429164													
C;Genetics: C;Gene: NRG3													
Query Match 100.0%; Score 277; DB 2; Length 713;													
Best Local Similarity 100.0%; Pred. No. 4.7e-24; Mismatches 0; Indels 0; Gaps 0;													
Matches 47; Conservative													
RESULT 2													
Query Match 100.0%; Score 277; DB 2; Length 713;													
C;Species: Homo sapiens (man)													
C;Accession: T4447													
R;Wen, D.; Suggs, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, T.; Mol. Cell. Biol. 14, 1909-1919, 1994													
A;Title: structural and functional aspects of the multiplicity of Neu differentiation													
A;Reference number: A56210; NID:9158863													
A;Accession: T44405													
A;Status: preliminary; translated from GB/EMBL/DDJB													
A;Molecule type: mRNA													
A;Residues: 1-125 <RHS>													
A;Cross-references: EMBL:002327; NID:9408404; PIDN:AAA1952.1; PID:9408405													
Query Match 41.0%; Score 113.5; DB 2; Length 125;													
Best Local Similarity 34.8%; Pred. No. 5.1e-06; Mismatches 15; Indels 1; Gaps 1;													
Matches 16; Conservative 14; Mismatches 15; Indels 1; Gaps 1;													
ALIGNMENTS													
Query Match 100.0%; Score 277; DB 2; Length 713;													
C;Species: <b>Mus musculus</b> (house mouse)													
C;Accession: T4447													
R;Zhang, D.; Sliwkowski, M.X.; Mark, M.; Frantz, G.; Alita, R.; Sun, Y.; Hillan, K.													
Proc. Natl. Acad. Sci. U.S.A. 94, 9562-9567, 1997													
A;Title: Neuregulin-3 (NRG3) - A novel tissue-enriched protein that binds and													
A;Reference number: 222773; NID:97420720													
A;Accession: T4447													
A;Status: preliminary; translated from GB/EMBL/DBJ													
A;Molecule type: mRNA													
A;Residues: 1-113 <2HA>													
A;Cross-references: EMBL:AF010130; NID:92429163; PIDN:AB70914.1; PID:92429164													
Query Match 100.0%; Score 277; DB 2; Length 713;													
C;Species: <b>Mus musculus</b> (house mouse)													
C;Accession: T4447													
R;Zhang, D.; Sliwkowski, M.X.; Mark, M.; Frantz, G.; Alita, R.; Sun, Y.; Hillan, K.													
Proc. Natl. Acad. Sci. U.S.A. 94, 9562-9567, 1997													
A;Title: Neuregulin-3 (NRG3) - A novel tissue-enriched protein that binds and													
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A;Status: preliminary; translated from GB/EMBL/DBJ													
A;Molecule type: mRNA													
A;Residues: 1-113 <2HA>													
A;Cross-references: EMBL:AF010130; NID:92429163; PIDN:AB70914.1; PID:92429164													
Query Match 100.0%; Score 277; DB 2; Length 713;													

## RESULT 3

I38404  
neu differentiation factor - human

C:Species: Homo sapiens (man) C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 05-Nov-1999

C:Accession: I38404  
C:Title: Structural and functional aspects of the multiplicity of Neu differentiation fa

A:Reference number: A56210; MUID:94158863

A:Accession: I38404  
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-462 <RES>  
A:Cross-references: EMBL:U02326; NID:9408402; PIDN:AAA19951.1; PID:9408403

Query Match  
Best Local Similarity 41.0%; Score 113.5; DB 2; Length 462;  
Matches 16; Conservative 14; Mismatches 15; Indels 1; Gaps 1;

QY 1 HFRPCRDQLAYCLNDGECFTVETLTSKHK-CRCKEGYQGVRCQ 45  
DB 178 HLVCAEKEKTFCVNGGECFVVKDLNSPNSRVLCKCQPGFTGARCTE 223

RESULT 4  
Av3273

hergulin precursor, splice form alpha - human  
N:Alternate names: breast cancer cell differentiation factor p45; Neu differentiation fa  
C:Species: Homo sapiens (man) C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 11-Jan-2000  
C:Accession: A43273; A48498; A81155  
R: Holmes, W.E.; Sliwowski, M.X.; Akita, R.W.; Henzel, W.J.; Lee, J.; Park, J.W.; Yansur  
Science 256, 1205-1210, 1992

A:Title: Identification of hergulin, a specific activator of p185(erbb2).

A:Reference number: A43273; MUID:92271253

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Residues: 1-640 <HOL>

A:Experimental source: breast tumor cell line, MDA-MB-231, ATCC HIB 26

A:Note: sequence extracted from NCBI backbone (NCBIP:103250)

R: Culouscou, J.M.; Plowman, G.D.; Carlton, G.W.; Green, J.M.; Shoyab, M.

J. Biol. Chem. 268, 18407-18410, 1993

A:Title: Characterization of a breast cancer cell differentiation factor that specifical

A:Reference number: A48498; MUID:93366731

A:Residues: 20-21, X, 23-24, 'XK', 27-28 <CUL>

A:Cross-references: EMBL:U02316; NID:9408382; PIDN:AAA19941.1; PID:9408383

A:Accession: I61117  
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-422, 'H', 'NL' 637-638, 'ELRNNAKARYSKMOTLSATHLRPSSITHLGFL' <RE4>

A:Accession: I61124  
A:Cross-references: EMBL:U02317; NID:9408384; PIDN:AAA19942.1; PID:9408385

A:Accession: 1-422 <RES>  
A:Cross-references: EMBL:U02324; NID:9408398; PIDN:AAA19949.1; PID:9408399

A:Accession: A38220; MUID:92257596

A:Title: Neu differentiation factor: a transmembrane glycoprotein containing an EGF

A:Reference number: A38220; MUID:92257596

A:Status: preliminary

A:Cross-references: EMBL:U02324; NID:9408398; PIDN:AAA19949.1; PID:9408399

A:Accession: A38220; MUID:92257596

A:Residues: 1-422 <WEN>

A:Note: sequence extracted from NCBI backbone (NCBIN:101767, NCBIP:101768)

C:Superfamily: unassigned EGF-related proteins; EGF homology

Query Match  
Best Local Similarity 40.3%; Score 111.5; DB 2; Length 639;  
Matches 16; Conservative 13; Mismatches 16; Indels 1; Gaps 1;

QY 1 HFRPCRDQLAYCLNDGECFTVETLTSKHK-CRCKEGYQGVRCQ 45  
DB 178 HLVCAEKEKTFCVNGGECFVVKDLNSPNSRVLCKCQPGFTGARCTE 223

## RESULT 5

I61719  
neu differentiation factor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Accession: I61719; I61723; I61724; A36720  
C:Title: Structural and functional aspects of the multiplicity of Neu differentiatio

A:Reference number: A56210; MUID:94158863

A:Accession: I61719  
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-639 <RES>

A:Cross-references: EMBL:U02319; NID:9408388; PIDN:AAA19944.1; PID:9408397

A:Accession: I61716  
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Cross-references: EMBL:U02316; NID:9408382; PIDN:AAA19941.1; PID:9408383

A:Accession: I61117  
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-639 <HOL>

A:Cross-references: EMBL:U02317; NID:9408384; PIDN:AAA19942.1; PID:9408385

A:Accession: 1-422 <RES>

A:Cross-references: EMBL:U02324; NID:9408398; PIDN:AAA19949.1; PID:9408399

A:Accession: A38220; MUID:92257596

A:Title: Neu differentiation factor: a transmembrane glycoprotein containing an EGF

A:Reference number: A38220; MUID:92257596

A:Status: preliminary

A:Cross-references: EMBL:U02324; NID:9408398; PIDN:AAA19949.1; PID:9408399

A:Accession: A38220; MUID:92257596

A:Residues: 1-422 <WEN>

A:Note: sequence extracted from NCBI backbone (NCBIN:101767, NCBIP:101768)

C:Superfamily: unassigned EGF-related proteins; EGF homology

Query Match  
Best Local Similarity 40.3%; Score 111.5; DB 2; Length 639;  
Matches 16; Conservative 13; Mismatches 16; Indels 1; Gaps 1;

QY 1 HFRPCRDQLAYCLNDGECFTVETLTSKHK-CRCKEGYQGVRCQ 45  
DB 178 HLVCAEKEKTFCVNGGECFVVKDLNSPNSRVLCKCQPGFTGARCTE 223

## RESULT 6

S02676  
hergulin isoform alpha 2 - human (fragments)

N:Alternate names: differentiation factor neu isoform alpha 2

C:Species: Homo sapiens (man)

C:Accession: S62676  
C:Title: Isoforms, Isolation and structural characterization of recombinant human neu differer

A:Reference number: S62676; MUID:96139341

A:Accession: S62676  
A:Status: preliminary

A:Residues: 1-67-161-730-31-38;39-58;59-92;93-120;121-125 <HAR>

A:Cross-references: EMBL:U02326; OMIM:142445

C:Superfamily: unassigned EGF-related proteins; EGF homology

C:Keywords: alternative splicing; glycoprotein

Query Match  
Best Local Similarity 41.0%; Score 113.5; DB 2; Length 640;  
Matches 16; Conservative 34-8a; Pred. No. 2.1e-05; Indels 1; Gaps 1;

QY 1 HFRPCRDQLAYCLNDGECFTVETLTSKHK-CRCKEGYQGVRCQ 45  
DB 178 HLVCAEKEKTFCVNGGECFVVKDLNSPNSRVLCKCQPGFTGARCTE 223

Query Match 38.1%; Score 105.5; DB 2; Length 125;  
Best Local Similarity 32.6%; Pred. No. 4.2e-05;  
Matches 15; Conservative 14; Mismatches 16; Indels 1; Gaps 1;

Qy 1 HFKPCRDQLAYCLNQGECFVIELTGSHKH-CRKKEGYQVRCQD 45  
Db 75 HLVCAEKEKTFCVNGGECFVNKGDKLNSPNSVLCCKCQPFQGARCT 120

RESULT 7  
138408  
neu differentiation factor - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000  
C;Accession: I38408  
R;Wen, D.; Sugunan, S. V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A.M.; Mol, Cell. Biol. 14, 1909-1919, 1994  
A;Title: Structural and functional aspects of the multiplicity of Neu differentiation factor  
A;Reference number: A56210; M01D:9158863  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: mRNA  
A;Residues: 1-175 <RBS>  
A;Cross-references: EMBL:U02330; PIDN:9408410; PIDN:AAA19955.1; PID:9408411  
C;Superfamily: unassigned EGF-related proteins; EGF homology F;110-155/Domain: EGF homology <EGF>

Query Match 37.7%; Score 104.5; DB 2; Length 175;  
Best Local Similarity 31.2%; Pred. No. 7.3e-05;  
Matches 15; Conservative 14; Mismatches 18; Indels 1; Gaps 1;

Qy 1 HFKPCRDQLAYCLNQGECFVIELTGSHKH-CRKKEGYQVRCQD 47  
Db 112 HLVCAEKEKTFCVNGGECFVNKGDKLNSPNSVLCCKCQPFQGARCT 159

RESULT 8  
S32359  
glial growth factor - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 19-May-1997 #sequence\_revision 01-Aug-1997 #text\_change 11-Jan-2000  
C;Accession: S32359  
R;Marchlioni, M.A.; Goodearl, A.D.J.; Chen, M.S.; Birmingham-McDonogh, O.; Kirk, C.; Hertog, I.; Davis, J.B.; Hsuan, J.J.; Totty, N.F.; Otsu, M.; McBurney, R.N.; Waterfield, M.; Nature 362, 312-318, 1993  
A;Title: Glial growth factors are alternatively spliced erbB2 ligands expressed in the retina and brain  
A;Reference number: S32357; M01D:93205115  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-241 <RBS>  
A;Cross-references: GB:U112259; NID:9289413; PIDN:AAA30540.1; PID:9289414  
C;Superfamily: unassigned EGF-related proteins; EGF homology F;182-221/Domain: EGF homology <EGF>

Query Match 37.7%; Score 104.5; DB 2; Length 241;  
Best Local Similarity 31.2%; Pred. No. 9.6e-05;  
Matches 15; Conservative 14; Mismatches 18; Indels 1; Gaps 1;

Qy 1 HFKPCRDQLAYCLNQGECFVIELTGSHKH-CRKKEGYQVRCQD 47  
Db 178 HLVCAEKEKTFCVNGGECFVNKGDKLNSPNSVLCCKCQPFQGARCT 225

RESULT 10  
A56943  
sensory/motor neuron-derived factor - human  
C;Species: Homo sapiens (man)  
C;Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 11-Jan-2000  
C;Accession: A56943  
R;Ho, W.H.; Armanini, M.P.; Nijhuis, A.; Phillips, H.S.; Oshiroff, P.L.; J. Biol. Chem. 270, 14523-14532, 1995  
A;Title: sensory and motor neuron-derived factor. A novel heparin variant highly conserved in the extracellular domain  
A;Reference number: A56943; M01D:95301541  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-295 <RBS>  
A;Cross-references: GB:U141827; NID:9862422; PIDN:AMC41764.1; PID:9862423  
C;Superfamily: unassigned EGF-related proteins; EGF homology F;237-276/Domain: EGF homology <EGF>

Query Match 37.7%; Score 104.5; DB 2; Length 296;  
Best Local Similarity 31.2%; Pred. No. 0.00011;  
Matches 15; Conservative 14; Mismatches 18; Indels 1; Gaps 1;

Qy 1 HFKPCRDQLAYCLNQGECFVIELTGSHKH-CRKKEGYQVRCQD 47  
Db 233 HLVCAEKEKTFCVNGGECFVNKGDKLNSPNSVLCCKCQPFQGARCT 280

RESULT 11  
S32357  
glial growth factor - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 11-Jan-2000  
C;Accession: S32357  
R;Marchlioni, M.A.; Goodearl, A.D.J.; Chen, M.S.; Birmingham-McDonogh, O.; Kirk, C.; Hertog, I.; Davis, J.B.; Hsuan, J.J.; Totty, N.F.; Otsu, M.; McBurney, R.N.; Waterfield, M.; Nature 362, 312-318, 1993  
A;Title: Glial growth factors are alternatively spliced erbB2 ligands expressed in the retina and brain  
A;Reference number: S32357; M01D:93205115  
A;Accession: S32357  
A;Status: preliminary  
A;Molecule type: mRNA

A;Residues: 1-422 <RES>  
 A;Cross-references: GB:Li2260; NID:9292047; PIDN:AB59622.1; PID:9292048  
 C;Superfamily: unassigned EGF-related proteins; EGF homology <EGF>  
 F;363-402/Domain: EGF homology <EGF>  
 Query Match  
 Best Local Similarity 37.7%; Score 104.5; DB 2; Length 422;  
 Matches 15; Conservative 14; Mismatches 18; Indels 1; Gaps 1;  
 Qy 1 HFKPCRDIDLAYCLNDGCFVIELTGSKH-CRCKEGYQGRCDQFL 47  
 Db 359 HLVKCAEKEKTFCVNGGECFMVKDLNSPRLCKCPNEFTGDRQNYV 406  
 RESULT 12  
 C43273  
 heregulin precursor, splice form beta-2 - human  
 C;Species: Homo sapiens (man)  
 C;Accession: C43273; #sequence\_revision 31-Dec-1993 #text\_change 17-Nov-2000  
 C;Accession: C43273; #sequence\_revision 31-Dec-1993 #text\_change 17-Nov-2000  
 A;Title: Identification of heregulin, a specific activator of p185(erbb2).  
 A;Accession: C43273  
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A;Molecule type: mRNA  
 A;Residues: 1-637 <HOL>  
 R;Wen, D.; Suggs, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A.M.;  
 Mol. Cell. Biol. 14, 1909-1919, 1994  
 A;Title: Structural and functional aspects of the multiplicity of Neu differentiation fa  
 A;Reference number: A56210; MUID:94158863  
 A;Accession: I38407  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 119-405 <RES>  
 A;Cross-references: EMBL:U02329; NID:9408408; PIDN:AAA19954.1; PID:9408409  
 C;Genetics:  
 A;Gene: GDB:HGL  
 A;Cross-references: GDB:132656; OMIM:142445  
 A;Map position: 8p22-8p11  
 C;Superfamily: unassigned EGF-related proteins; EGF homology <EGF>  
 C;Keywords: alternative splicing  
 F;162-221/Domain: EGF homology <EGF>  
 Query Match  
 Best Local Similarity 37.7%; Score 104.5; DB 2; Length 637;  
 Matches 15; Conservative 14; Mismatches 18; Indels 1; Gaps 1;  
 Qy 1 HFKPCRDIDLAYCLNDGCFVIELTGSKH-CRCKEGYQGRCDQFL 47  
 Db 178 HLVKCAEKEKTFCVNGGECFMVKDLNSPRLCKCPNEFTGDRQNYV 225  
 RESULT 13  
 B43273  
 heregulin, splice form beta 1 - human  
 C;Species: Homo sapiens (man)  
 C;Accession: B43273; #sequence\_revision 31-Dec-1993 #text\_change 17-Nov-2000  
 C;Accession: B43273; I38406  
 R;Holmes, W.E.; Sliwkowski, M.X.; Akita, R.W.; Henzel, W.J.; Lee, J.; Park, J.W.; Yansur  
 Science 265, 1205-1210, 1992  
 A;Title: Identification of heregulin, a specific activator of p185(erbb2).  
 A;Reference number: A43273; MUID:92271253  
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A;Molecule type: mRNA  
 A;Residues: 1-645 <HOL>  
 R;Wen, D.; Suggs, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A.M.;  
 Mol. Cell. Biol. 14, 1909-1919, 1994  
 A;Title: Structural and functional aspects of the multiplicity of Neu differentiation fa  
 A;Accession: I38406  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Cross-references: EMBL:U02321; NID:9408392; PIDN:AAA19946.1; PID:9408393  
 A;Accession: I61720  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-230 <RES>  
 A;Cross-references: EMBL:U02318; NID:9408386; PIDN:AAA19943.1; PID:9408387  
 A;Accession: I61721  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-444; 'A', 446-636 <RES>  
 A;Cross-references: EMBL:U02321; NID:9408392; PIDN:AAA19946.1; PID:9408393  
 A;Accession: I61720  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-238; 386, 'V', 388, 'TR', 391 <RES>  
 A;Cross-references: EMBL:U02320; NID:9408390; PIDN:AAA19945.1; PID:9408391  
 C;Superfamily: unassigned EGF-related proteins; EGF homology <EGF>  
 F;182-221/Domain: EGF homology <EGF>  
 Query Match  
 Best Local Similarity 37.7%; Score 104.5; DB 2; Length 645;  
 Matches 15; Conservative 14; Mismatches 18; Indels 1; Gaps 1;  
 Qy 1 HFKPCRDIDLAYCLNDGCFVIELTGSKH-CRCKEGYQGRCDQFL 47  
 Db 178 HLVKCAEKEKTFCVNGGECFMVKDLNSPRLCKCPNEFTGDRQNYV 225  
 RESULT 14  
 A56210  
 neu differentiation factor - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Accession: A56210  
 R;Wen, D.; Suggs, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A;Title: Structural and functional aspects of the multiplicity of Neu differentiatic  
 A;Reference number: A56210; MUID:94158863  
 A;Accession: A56210  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-230 <RES>  
 A;Cross-references: EMBL:U02315; NID:9408380; PIDN:AAA19940.1; PID:9408381  
 C;Superfamily: unassigned EGF-related proteins; EGF homology <EGF>  
 Query Match  
 Best Local Similarity 37.0%; Score 102.5; DB 2; Length 230;  
 Matches 15; Conservative 31; Mismatches 19; Indels 1; Gaps 1;  
 Qy 1 HFKPCRDIDLAYCLNDGCFVIELTGSKH-CRCKEGYQGRCDQFL 47  
 Db 167 HLVKCAEKEKTFCVNGGECFMVKDLNSPRLCKCPNEFTGDRQNYV 214  
 RESULT 15  
 B43273  
 neu differentiation factor - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Accession: I61718; #sequence\_revision 29-May-1998 #text\_change 17-Nov-2000  
 C;Accession: I61718; I61721; I61720  
 R;Wen, D.; Suggs, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A;Title: Structural and functional aspects of the multiplicity of Neu differentiatic  
 A;Reference number: A56210; MUID:94158863  
 A;Accession: I61718  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-636 <RES>  
 A;Cross-references: EMBL:U02318; NID:9408386; PIDN:AAA19943.1; PID:9408387  
 A;Accession: I61721  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-444; 'A', 446-636 <RES>  
 A;Cross-references: EMBL:U02321; NID:9408392; PIDN:AAA19946.1; PID:9408393  
 A;Accession: I61720  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-238; 386, 'V', 388, 'TR', 391 <RES>  
 A;Cross-references: EMBL:U02320; NID:9408390; PIDN:AAA19945.1; PID:9408391  
 C;Superfamily: unassigned EGF-related proteins; EGF homology <EGF>

F:182-221/Domain: EGF homology <EGF>

Query Match 37.0%; Score 103.5; DB 2; Length 636;  
 Best Local Similarity 31.2%; Pred. No. 0.00038;  
 Matches 15; Conservative 13; Mismatches 19; Indels 1; Gaps 1  
 OY 1 HFKPCRDQLAYCLNDGBCFVPIIHLTGSKH-H-CRKCEGYQVRCRDOFL 47  
 Db 178 HLIKCAEKEKTFVCUNGBCFTVKDLSNPSSRYLCKCPNPEITGDRQNYV 225

Search completed: November 7, 2002, 10:00:27  
Job time : 19 secs

GenCore version 5.1.3  
 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model  
 Run on: November 7, 2002, 09:59:04 ; Search time 30 Seconds  
 (without alignments)  
 174.016 Million cell updates/sec

Title: US-09-480-977-4  
 Perfect score: 277  
 Sequence: 1 HFKPCRDKLAYCLNDGCF..... SHKHCRCRKEGYQCVRCQFL 47

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq403802:  
 1: /SIDS1/gcdata/geneseq/geneseq/geneseq -emb1/AA1980.DAT: \*  
 2: /SIDS1/gcdata/geneseq/geneseq/geneseq -emb1/AA1981.DAT: \*  
 3: /SIDS1/gcdata/geneseq/geneseq/geneseq -emb1/AA1982.DAT: \*  
 4: /SIDS1/gcdata/geneseq/geneseq -emb1/AA1983.DAT: \*  
 5: /SIDS1/gcdata/geneseq/geneseq -emb1/AA1984.DAT: \*  
 6: /SIDS1/gcdata/geneseq/geneseq -emb1/AA1985.DAT: \*  
 7: /SIDS1/gcdata/geneseq/geneseq -emb1/AA1986.DAT: \*  
 8: /SIDS1/gcdata/geneseq/geneseq -emb1/AA1987.DAT: \*  
 9: /SIDS1/gcdata/geneseq/geneseq/geneseq -emb1/AA1988.DAT: \*  
 10: /SIDS1/gcdata/geneseq/geneseq/geneseq -emb1/AA1989.DAT: \*  
 11: /SIDS1/gcdata/geneseq/geneseq/geneseq -emb1/AA1990.DAT: \*  
 12: /SIDS1/gcdata/geneseq/geneseq/geneseq -emb1/AA1991.DAT: \*  
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 15: /SIDS1/gcdata/geneseq/geneseq/geneseq -emb1/AA1994.DAT: \*  
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 21: /SIDS1/gcdata/geneseq/geneseq/geneseq -emb1/AA2000.DAT: \*  
 22: /SIDS1/gcdata/geneseq/geneseq/geneseq -emb1/AA2001.DAT: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	277	100.0	47	20 AAW97622 Human neuregulin r
2	277	100.0	157	20 AAY05451 Human heregulin-11
3	277	100.0	350	20 AAW97620 Human neuregulin r
4	277	100.0	362	20 AAW97620 Mouse neuregulin r
5	277	100.0	696	20 AAW97619 Human neuregulin r
6	277	100.0	713	20 AAW97617 Mouse neuregulin r
7	277	100.0	720	20 AY03452 Human heregulin-11
8	277	100.0	720	20 AAW97618 Human neuregulin r
9	116.5	43.1	52	17 AAW05182 Neu differentiation
10	116.5	42.1	52	21 AAB12602 Human NRP EGF-like
11	116.5	42.1	52	21 AY69983 NDF/hereregulin prot

## ALIGNMENTS

RESULT ID	DB ID	Description
1	AAW97622	Human neuregulin related ligand NRG3 EGF-like domain.
2	AAW97622	Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; epidermal growth factor; EGF; immunoadhesin.
3	XX	Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; epidermal growth factor; EGF; immunoadhesin.
4	XX	Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; epidermal growth factor; EGF; immunoadhesin.
5	XX	Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; epidermal growth factor; EGF; immunoadhesin.
6	XX	Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; epidermal growth factor; EGF; immunoadhesin.
7	XX	Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; epidermal growth factor; EGF; immunoadhesin.
8	XX	Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; epidermal growth factor; EGF; immunoadhesin.
9	XX	Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; epidermal growth factor; EGF; immunoadhesin.
10	XX	Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; epidermal growth factor; EGF; immunoadhesin.
11	XX	Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; epidermal growth factor; EGF; immunoadhesin.
12	XX	Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; epidermal growth factor; EGF; immunoadhesin.
13	XX	Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; epidermal growth factor; EGF; immunoadhesin.
14	XX	Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; epidermal growth factor; EGF; immunoadhesin.
15	XX	Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; epidermal growth factor; EGF; immunoadhesin.
16	XX	Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; epidermal growth factor; EGF; immunoadhesin.
17	XX	Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; epidermal growth factor; EGF; immunoadhesin.
18	XX	Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; epidermal growth factor; EGF; immunoadhesin.
19	XX	Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; epidermal growth factor; EGF; immunoadhesin.
20	XX	Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; epidermal growth factor; EGF; immunoadhesin.
21	XX	Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; epidermal growth factor; EGF; immunoadhesin.

Neu differentiation  
 EGFL2. AAR46918;  
 EGFL2. AAR55659;  
 Human epidermal 11  
 EGFL2. Not specif  
 EGFL6. AAR6922;  
 EGFL6. AAR5662;  
 Human epidermal 11  
 EGFL5. Not specif  
 Epidermal growth f  
 Epidermal growth f  
 EGFL5. AAR6921;  
 EGFL5. AAR55662;  
 Human NDF-alpha3 C  
 Human NRG1 gene Ne  
 Human NRG1 gene Ne  
 GGF2BPP2.CDS prote  
 GGF2BPP2. Bos tau  
 GGF2BPP2. Bos tau  
 putative bovine gl  
 Bovine neuregulin  
 GGF2BPP2. Bos tau  
 GGF2BPP2. Bos tau  
 Bovine glial cell  
 Human neuregulin G

Neu differentiation  
 EGFL2. AAR46918;  
 EGFL2. AAR55659;  
 Human epidermal 11  
 EGFL2. Not specif  
 EGFL6. AAR6922;  
 EGFL6. AAR5662;  
 Human epidermal 11  
 EGFL5. Not specif  
 Epidermal growth f  
 Epidermal growth f  
 EGFL5. AAR6921;  
 EGFL5. AAR55662;  
 Human NDF-alpha3 C  
 Human NRG1 gene Ne  
 Human NRG1 gene Ne  
 GGF2BPP2.CDS prote  
 GGF2BPP2. Bos tau  
 GGF2BPP2. Bos tau  
 putative bovine gl  
 Bovine neuregulin  
 GGF2BPP2. Bos tau  
 GGF2BPP2. Bos tau  
 Bovine glial cell  
 Human neuregulin G

New isolated neuregulin related ligand-3 - used to develop products for treating nervous system disorders, e.g. stroke, ischaemia,

PT Infection, malignancy, Alzheimer's disease or Down's syndrome

XX

PS Claim 30; Page 64; 101pp; English.

XX

CC This is the epidermal growth factor (EGF)-like domain of human

CC neuregulin related ligand NRG3 (see also AAW97618), a novel member of

CC the EGF-like family of protein ligands that binds to the ErbB4

CC receptor and activates ErbB4 receptor tyrosine phosphorylation.

CC The EGF-like domain of NRG3 is distinct from the EGF-like domains

CC of NRG1 and NRG2. The invention provides human and murine

CC polypeptides (see also AAW97617) that have at least 75% homology to

CC the NRG3 EGF-like domain, as well as expression vectors, host cells

CC and methods for the recombinant production of novel NRG3s. The

CC NRG3 polypeptides and polynucleotides and can be used to enhance

CC the survival, proliferation or differentiation of cells having the

CC ErbB4 receptor *in vivo* and *in vitro*. They can be used to prevent

CC or treat damage to a nerve or damage to other NRG3-expressing or

CC NRG3-responsive cells, e.g. brain, heart, or kidney cells. In

CC particular, they can be used to treat diseases which involve neural

CC cell growth such as demyelination, or damage or loss of glial cells

CC (e.g. multiple sclerosis). They can be used to treat patients whose

CC nervous system has been damaged by e.g. trauma, surgery, stroke,

CC ischaemia, infection, metabolic disease, nutritional deficiency,

CC malignancy, or toxic agents.

CC NRG3 can also be used to treat

CC motor neuron disorders such as amyotrophic lateral sclerosis (Lou

CC Gehrig's disease), Bell's palsy, conditions involving spinal

CC muscular atrophy or paralysis, neurodegenerative disorders such as

CC Alzheimer's disease, Parkinson's disease, epilepsy, multiple

CC sclerosis, Huntington's chorea, Down's syndrome, nerve deafness,

CC and Meniere's disease. They can also be used to treat neuropathies

CC associated with systemic disease including Charcot-Marie-Tooth disease,

CC Refsum's disease, abetalipoproteinemia, Tangier disease, Krabbe's

CC disease, metachromatic leukodystrophy, Fabry's disease and

CC Dejerine-Sottas syndrome, to treat disease of skeletal muscle of

CC smooth muscle, such as muscular dystrophy or diseases caused by

CC skeletal or smooth muscle wasting. The products can also be used

CC for detection, diagnosis, for the production of transgenic or

CC knockout animals or for drug screening. A claimed immunoadhesin

CC sequence, comprising the human NRG3 EGF-like domain fused to an immunoglobulin

CC

SQ Sequence 47 AA;

XX

Query Match 100.0%; Score 277; DB 20;

Best Local Similarity 100.0%; Pred. No. 2.5e-21; Length 47;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC

OY 1 HFKPCRDLDAYCLNDGECFVLTGSHKICRKCKEGYQGVRCDFL 47

Db 31 HFKPCRDLDAYCLNDGECFVLTGSHKICRKCKEGYQGVRCDFL 77

CC

RESULT 3

AAW97621

ID AAW97621 standard; Protein; 360 AA.

XX

AC AAW97621;

XX

DT 10-MAY-1999 (first entry)

XX

DE Human neuregulin related ligand NRG3 extracellular domain.

XX

KW Neuregulin related ligand; NRG3; hNG3BL; human; ErbB4 receptor;

KW signal transduction; nervous system disorder; neurodegeneration;

KW neuropathy; therapy; diagnosis.

XX

OS Homo sapiens.

XX

PN WO9902681-A1.

XX

PP 21-JAN-1999.

XX

PF 30-JUN-1998; 98WO-US13411.

XX

PR 24-JUL-1997; 97US-0899437.

PR 09-JUL-1997; 97US-0052019.

XX

PA (GETH ) GENENTECH INC.

XX

PT Godowski PJ, Mark MR, Zhang D;

XX

DR WPI; 1999-120882/10.

XX

PT New isolated neuregulin related ligand-3 - used to develop products  
PT for treating nervous system disorders, e.g. stroke, ischaemia,  
PT infection, malignancy, Alzheimer's disease or Down's syndrome

XX

PS Claim 5(a); Page 69-70; 101pp; English.

XX





CC human and murine NRG3 polypeptides (see also AAW97618), expression vectors, host cells and methods for the recombinant production of NRG3s. The NRG3 polypeptides and polynucleotides and can be used to enhance the survival, proliferation or differentiation of cells having the Erbb4 receptor in vivo and in vitro. They can be used to prevent or treat damage to a nerve or damage to other NRG3-expressing or NRG3-responsive cells, e.g. brain, heart, or kidney cells. In particular, they can be used to treat diseases which involve neural cell growth such as demyelination, or damage or loss of glial cells (e.g. multiple sclerosis). They can be used to treat patients whose nervous system has been damaged by e.g. trauma, surgery, stroke, ischaemia, infection, metabolic disease, nutritional deficiency, malignancy, or toxic agents. NRG3 can also be used to treat motor neuron disorders such as amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, conditions involving spinal muscular atrophy or paralysis, neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, and Meniere's disease. They can also be used to treat neuropathies associated with systemic disease including post-polio syndrome, hereditary neuropathies including Charcot-Marie-Tooth disease, Refsum's disease, abetalipoproteinemia, Tangier disease, Krabbe's disease, metachromatic leukodystrophy, Fabry's disease and Dejerine-Sottas syndrome, to treat disease of skeletal muscle of smooth muscle, such as muscular dystrophy or diseases caused by skeletal or smooth muscle wasting. The products can also be used for detection, diagnosis, for the production of transgenic or knockout animals or for drug screening.

XX Sequence: 713 AA;

SO Query Match 100.0%; Score 277; DB 20; Length 713; Best Local Similarity 100.0%; Pred. No. 3.1e-20; Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKPCKRDKDYLAYCLNGECLGECFVIETLGSHKHCRCKEGYQGVRCDQFL 47

Db 288 HKPCKRDKDYLAYCLNGECLGECFVIETLGSHKHCRCKEGYQGVRCDQFL 334

RESULT 7

ID AAY05452 standard; Protein: 720 AA.

XX AAY05452;

AC AAY05452;

CC 06-JUL-1999 (first entry)

DE Human heregulin-like factor sequence.

KW Human heregulin-like factor; HGF; cell growth regulator; diagnosis; neural system disorder; cancer.

XX Homo sapiens.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Domain 1..360

FT /note= "extracellular domain," specifically claimed in Claim 5(a).

FT Region 66..91

FT /note= "hydrophobic region"

FT Region 101..284

FT /note= "mucin-like Ser/Thr-rich region," contains 285..354 sites for O-linked glycosylation.

FT Domain /note= "EGF-like domain"

FT Domain 356..394

FT /note= "transmembrane domain"

PN WO9902681-A1.

XX 21-JAN-1999.

XX 30-JUN-1998; 98WO-013411.

XX 24-JUL-1997; 97US-0899437.

XX 09-JUL-1997; 97US-0052019.

PA (GETH ) GENENTECH INC.

XX

PI Godowski PJ, Mark MR, Zhang D;

XX DR WPI; 1999-120882/10.

XX DR N-PSDB; AAX0698B.

XX

PT New isolated heregulin-related ligand-3 - used to develop products for treating nervous system disorders, e.g. stroke, ischaemia, infection, malignancy, Alzheimer's disease or Down's syndrome

PT

PT New isolated heregulin-like factor - used to develop products for the diagnosis and treatment of disorders involving regulation of cell growth, particularly cancers

PT

XX Disclosure; Page 97-99; 118pp; English.

PS

XX

CC This sequence is the human heregulin-like factor (HLF) of the invention. The HLF is involved in the regulation of cell growth. Detection of different levels of expression of the Hlf gene can be used for the diagnosis of disorders, e.g. in the neural system. In particular, detection of different levels of HLF gene expression in cells or body fluid of an individual can be used for diagnosing cancer. The products can also be used in the treatment of disorders involving abnormal levels of HLF activity.

XX Sequence 720 AA;

SO Query Match 100.0%; Score 277; DB 20; Length 720; Best Local Similarity 100.0%; Pred. No. 3.1e-20; Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKPCKRDKDYLAYCLNGECLGECFVIETLGSHKHCRCKEGYQGVRCDQFL 47

Db 286 HKPCKRDKDYLAYCLNGECLGECFVIETLGSHKHCRCKEGYQGVRCDQFL 332

RESULT 8

ID AAW97618

XX AAW97618 standard; Protein: 720 AA.

AC AAW97618;

XX DT 10-MAY-1999 (first entry)

XX Human neuregulin related ligand NRG3.

XX Neuregulin related ligand; NRG3; human; Erbb4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis.

XX

OS Homo sapiens.

FT Key Location/Qualifiers

FT Domain 1..360

FT /note= "extracellular domain," specifically claimed in Claim 5(a).

FT Region 66..91

FT /note= "hydrophobic region"

FT Region 101..284

FT /note= "mucin-like Ser/Thr-rich region," contains 285..354 sites for O-linked glycosylation.

FT Domain /note= "EGF-like domain"

FT Domain 356..394

FT /note= "transmembrane domain"

PN WO9902681-A1.

XX 21-JAN-1999.

XX 30-JUN-1998; 98WO-013411.

XX 24-JUL-1997; 97US-0899437.

XX 09-JUL-1997; 97US-0052019.

PA (GETH ) GENENTECH INC.

XX

PI Godowski PJ, Mark MR, Zhang D;

XX DR WPI; 1999-120882/10.

XX DR N-PSDB; AAX0698B.

XX

PT New isolated heregulin related ligand-3 - used to develop products for treating nervous system disorders, e.g. stroke, ischaemia, infection, malignancy, Alzheimer's disease or Down's syndrome

PT

PT

PS Claim 5(b); Page 66-69; 101pp; English.

XX

CC

XX  
 PR 06-APR-1995; 95US-0417640.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Cranahan JF, Hara S, Lu HS, Mayer JP, Yoshihaga SK;  
 XX  
 DR WPI; 1996-465022/46.  
 XX  
 PT Peptides(s) derived from neu differentiation factor/Heregulin  
 PT proteins - specifically from epidermal growth factor-like domain,  
 PT stimulate proliferation of colon epithelial cells and Schwann cells  
 XX  
 PS claim 1; Page 27; 37pp; English.  
 XX  
 CC The peptides AAW05182-W05185 are based on neu differentiation factor  
 CC (NDF)/heregulin alpha and beta form EGF-like domains in various factor  
 CC combinations. The peptides maintain the survival and proliferation of  
 CC Schwann cells and cause proliferation, growth and differentiation of  
 CC colon epithelial cells. Accordingly, they are useful to treat (in vitro  
 CC or in vivo) a disease or disorder of the colon (e.g. colitis or an  
 CC ulcer) or of the nervous system (e.g. nerve damage caused by trauma).  
 XX  
 SQ Sequence 52 AA;  
 XX  
 Query Match Best Local Similarity 42.1%; Score 116.5; DB 17; Length 52;  
 XX Matches 16; Conservative 15; Mismatches 16; Indels 1; Gaps 1;  
 XX  
 Qy 1 HFKPCRDKLAVCLNDEGCFVIETLNGSHHH-CRCKEGTGVQVDRFL 47  
 DB 2 HLYVKCAKEKTCFVNGGECFAVKDLSNPSVLCRCKQGFTGARCONVY 49  
 XX  
 RESULT 10  
 ID AAB12602  
 ID AAB12602 standard; Peptide; 52 AA.  
 XX  
 AC AAB12602;  
 XX  
 DR 09-NOV-2000 (first entry)  
 XX  
 DE Human NDF EGF-like domain derived peptide SEQ ID NO:1.  
 XX  
 KW Human; sensory epithelial cell; growth; stimulant; inner ear; EGF;  
 KW epithelial growth factor; NDF; heregulin; monoclonal antibody;  
 KW adult rat utricular epithelium.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6080845-A.  
 XX  
 PD 27-JUN-2000.  
 XX  
 PF 28-JAN-1999; 990US-0238182.  
 XX  
 PR 05-AUG-1998; 98US-0129549.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Carnahan JF;  
 XX  
 DR WPI; 2000-451229/39.  
 XX  
 PT Novel monoclonal antibody against adult rat utricular epithelium useful  
 PT in study and research with such organs and tissue  
 XX  
 XX  
 PS Example 1; Fig 1; 12pp; English.  
 XX  
 CC The present invention describes a monoclonal antibody (1) deposited with  
 CC the American Type Culture Collection under accession number HB-1258.  
 The antibodies are used in study and research with adult rat utricular

Query Match Best Local Similarity 100.0%; Score 277; DB 20; Length 720;  
 XX Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 Qy 1 HFKPCRDKLAVCLNDEGCFVIETLNGSHHH-CRCKEGTGVQVDRFL 47  
 DB 286 HFKPCRDKLAVCLNDEGCFVIETLNGSHHH-CRCKEGTGVQVDRFL 332  
 XX  
 RESULT 9  
 ID AAW05182  
 ID AAW05182 standard; peptide; 52 AA.  
 XX  
 AC AAW05182;  
 XX  
 DT 04-JUN-1997 (first entry)  
 XX  
 DE Neu differentiation factor/heregulin-alpha/beta form EGF-like domain.  
 XX  
 KW NDF; neu differentiation factor; heregulin; epidermal growth factor;  
 KW EGF; colon epithelial cell proliferation; Schwann cell; nerve;  
 KW damage; colitis; ulcer.  
 XX  
 OS Synthetic.  
 XX  
 PN WO96131599-A1.  
 XX  
 PD 10-OCT-1996.  
 XX  
 PT 27-MAR-1996; 96WO-US04262.

CC organs and tissues. The present sequence is a peptide derived from the epithelial growth factor (EGF) like domains of NDF-alpha and NDF-beta (members of the NDF/heregulin protein family, which is used in the exemplification of the present invention. The peptide acts as a growth stimulant for sensory epithelial cells of the inner ear.

XX SQ sequence 52 AA;

Query Match 42.1%; Score 116.5; DB 21; Length 52; Best Local Similarity 33.3%; Pred. No. 4.7e-05; Matches 16; Conservative 15; Mismatches 16; Indels 1; Gaps 1; Neu differentiation factor/heregulin-alpha form EGF-like domain.

ID AAW05184 standard; peptide; 52 AA.

ID AAW05184;

ID AAW

PR 10-AUG-1992; 92US-0927337.  
 PR 01-SEP-1992; 92US-0984085.  
 PR 29-JAN-1993; 93US-0011396.  
 XX  
 PA (CAMB-) CAMBRIDGE NEUROSCIENCE INC.  
 XX  
 PI Gwynne DI, Marchionni M, McBurney RN;  
 XX WPI; 1994-065731/08.  
 DR N-PSDB; AA058324.  
 XX  
 PT Glial growth factor DNA encoding numerous polypeptide factors used for inhibiting cell proliferation - for treating carcinoma and nervous disorders  
 XX  
 PS Disclosure; Fig 40; 178pp; English.  
 XX  
 CC The GGF coding segments include regions with BGF-like homology. These BGF-like domains can be required for the activation of mitogenesis in the binding reaction between GGF ligands and such domains in the erbB2 receptor. Pref. antiproliferative factors are those which lack these BGF-like domains.  
 XX  
 SQ Sequence - 63 AA:  
 XX  
 Query Match 41.0%; Score 113.5; DB 15; Length 63;  
 CC Best Local Similarity 34.8%; Pred. No. 0.00011;  
 CC Matches 16; Conservative 14; Mismatches 15; Indels 1; Gaps 1;  
 CC  
 QY 1 HFKPCRDQLAYCLNDGECFVIELTGGSHKH-CRCREGYQYGRCDQ 45  
 CC  
 DB 2 HLVKCAEKTFCVNGGECFVMKDLNSPNSPRYLCKCOPGFTGARCTE 47  
 XX  
 RESULT 14  
 XX  
 ID AAR55659  
 XX AAR55659 standard; Protein; 63 AA.  
 AC AAR55659;  
 XX  
 DT 28-JUL-1994 (first entry)  
 XX  
 DE EGFL2.  
 XX  
 AAR55659 standard; Protein; 63 AA.  
 XX  
 AC AAR55659;  
 XX  
 DT 28-JUL-1994 (first entry)  
 XX  
 DE EGFL2.  
 XX  
 KW Glial growth factor; heregulin; mitogenesis;  
 KW Schwann cell; tumour; central nervous system;  
 KW epidermal growth factor; BGF.  
 XX  
 PN W0940140-A.  
 XX  
 PD 06-JAN-1994.  
 XX  
 PP 29-JUN-1993; 93WO-US06228.  
 XX  
 PR 30-JUN-1992; 92US-0907138.  
 PR 03-SEP-1992; 92US-0940389.  
 PR 23-OCT-1993; 92US-0951713.  
 PR 24-MAR-1993; 93US-0036555.  
 XX  
 PA (CAMB-) CAMBRIDGE NEUROSCIENCE:  
 PA (LUDWIG) LUDWIG INST CANCER RES.  
 XX  
 PI Chen MS, Goodearl A, Hiles I, Marchionni M, Minghetti L;  
 PI Stroobant P, Waterfield M;  
 XX  
 DR WPI; 1994-025880/03.  
 DR N-PSDB; AA062843.  
 XX  
 PT Glial mitogenic polypeptide factors - useful for stimulating  
 PT glial cell mitogenesis and treating glial cell tumours  
 XX  
 PS Claim 53; Fig 39; 178pp; English.

XX  
 EGFL1, EGFL2, EGFL3, EGFL4, EGFL5 and EGFL6 are used for the stimulation of glial cell mitogenesis in vivo and in vitro.  
 XX  
 SQ Sequence - 63 AA:  
 XX  
 ID AAR67250  
 XX AAR67250 standard; Protein; 63 AA.  
 AC AAR67250;  
 XX  
 DT 15-AUG-1995 (first entry)  
 XX  
 DE Human epidermal like growth factor 2 (EGFL2).  
 XX  
 KW Epidermal like growth factor 2; mammalian muscle cell treatment; skeletal; cardiac; smooth; acetylcholine receptor deficiency; EGFL2.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09426298-A.  
 XX  
 PD 24-NOV-1994.  
 XX  
 PR 06-MAY-1994; 94WO-US050983.  
 XX  
 PR 06-MAY-1993; 93US-0059022.  
 PR 08-MAR-1994; 94US-0209204.  
 XX  
 PA (CAMB-) CAMBRIDGE NEUROSCIENCE.  
 PI Gwynne DI, Marchionni M, Sklar R;  
 XX  
 DR N-PSDB; AA074915.  
 XX  
 PT Treating mammalian muscle diseases and disorders - by admin. of  
 PT GGF2 and other specified polypeptide(s) which bind the p185erb2 receptor.  
 XX  
 PS Claim 34; Pages 148-149; 241pp; English.  
 XX  
 CC AAQ74915 encodes AAR67250 human epidermal like growth factor 2 (EGFL2).  
 CC The glial cell mitogenic activity of EGFL2 can be used to treat a variety of mammalian skeletal, cardiac and smooth muscle diseases, including acetylcholine receptor deficiency.  
 XX  
 SQ Sequence - 63 AA:  
 XX  
 Query Match 41.0%; Score 113.5; DB 16; Length 63;  
 CC Best Local Similarity 34.8%; Pred. No. 0.00011;  
 CC Matches 16; Conservative 14; Mismatches 15; Indels 1; Gaps 1;  
 CC  
 QY 1 HFKPCRDQLAYCLNDGECFVIELTGGSHKH-CRCREGYQYGRCDQ 45  
 CC  
 DB 2 HLVKCAEKTFCVNGGECFVMKDLNSPNSPRYLCKCOPGFTGARCTE 47  
 XX  
 Search completed: November 7, 2002, 09:59:44  
 Job time : 32 secs

GenCore - version 5.1.3  
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On protein - protein search, using sw model

Run on: November 7, 2002, 09:59:49 ; Search time 13 Seconds  
(without alignments)  
88.308 Million cell updates/sec

Title: US-09-480-977-4

Perfect score: 277  
Sequence: 1 HFKPCRDKDLAYCLNQECF . . . . . SHKHCRCCKBCYQGVRCQDFL 47

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A\_COMB\_pep:\*

2: /cgn2\_6/ptodata/1/1aa/5B\_COMB\_pep:\*

3: /cgn2\_6/ptodata/1/1aa/6A\_COMB\_pep:\*

4: /cgn2\_6/ptodata/1/1aa/6B\_COMB\_pep:\*

5: /cgn2\_6/ptodata/1/1aa/PCITUS\_COMB\_pep:\*

6: /cgn2\_6/ptodata/1/1aa/backfile1\_pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. Score Query Match Length DB ID Description

1 277 100.0 47 3 US-08-899-437-4 Sequence 4, Appl1

2 277 100.0 47 3 US-08-899-437-8 Sequence 8, Appl1

3 277 100.0 47 4 US-09-126-121-4 Sequence 4, Appl1

4 277 100.0 47 4 US-09-126-121-8 Sequence 8, Appl1

5 277 100.0 360 3 US-08-899-437-7 Sequence 7, Appl1

6 277 100.0 360 4 US-09-126-121-7 Sequence 7, Appl1

7 277 100.0 362 3 US-08-899-437-3 Sequence 3, Appl1

8 277 100.0 362 4 US-09-126-121-3 Sequence 3, Appl1

9 277 100.0 696 3 US-08-899-437-23 Sequence 23, Appl1

10 277 100.0 696 4 US-09-126-121-23 Sequence 23, Appl1

11 277 100.0 713 3 US-08-899-437-2 Sequence 2, Appl1

12 277 100.0 713 4 US-09-126-121-2 Sequence 2, Appl1

13 277 100.0 720 3 US-08-899-437-6 Sequence 6, Appl1

14 277 100.0 720 4 US-09-126-121-5 Sequence 6, Appl1

15 116.5 42.1 52 1 US-08-417-640A1 Sequence 1, Appl1

16 116.5 42.1 52 2 US-08-761-038-1 Sequence 1, Appl1

17 116.5 42.1 52 3 US-09-281821 Sequence 1, Appl1

18 113.5 41.0 49 3 US-08-899-437-14 Sequence 14, Appl1

19 113.5 41.0 49 4 US-03-126-121-14 Sequence 14, Appl1

20 113.5 41.0 50 3 US-08-753-007A12 Sequence 12, Appl1

21 113.5 41.0 50 4 US-08-398-496-12 Sequence 12, Appl1

22 113.5 41.0 52 1 US-08-417-640A3 Sequence 3, Appl1

23 113.5 41.0 52 2 US-08-761-038-3 Sequence 3, Appl1

24 113.5 41.0 54 1 US-08-179-481-111 Sequence 3, Appl1

25 113.5 41.0 63 3 US-08-341-018-62 Sequence 62, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-899-437-4  
; Sequence 4, Application US/08899437  
; Patent No. 6121415  
; GENERAL INFORMATION:  
; APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao  
; TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related  
; LIGands and Uses Therefor  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 Inch, 1.44 MB floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/899,437  
FILING DATE: 24-Jul-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Conley, Deirdre L.  
REGISTRATION NUMBER: 36,487  
REFERENCE/DOCKET NUMBER: P1084RL  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-2066  
TELEFAX: 650/952-8881  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 47 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
FEATURE:  
NAME/KEY: NRG3 EGF-like domain/amino acid seq.  
LOCATION: 1-47  
IDENTIFICATION METHOD:  
OTHER INFORMATION:

US-08-899-437-4

Query Match 100% ; Score 277; DB 3; Length 47;

Best Local Similarity 100% ; Pred. No. 1.3e-26;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HFKPCRDKDLAYCLNQECF . . . . . SHKHCRCCKBCYQGVRCQDFL 47

Db

1 HFKPCRDKDLYCLNDGECFVIETLIGSHKHCRCREGYQGVRCDQFL 47

RESULT 2

US-08-899-437-8

Sequence 8, Application US/08899437

; Patent No. 612415.

; GENERAL INFORMATION:

; APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao

; TITLE OF INVENTION: Erbb Receptor-Specific Neuregulin Related

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Winpatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/126,121

; FILING DATE: 30-Jul-1998

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Conley, Deidre L.

; REGISTRATION NUMBER: 36,487

; REFERENCE/DOCKET NUMBER: P1084R1D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/952-2066

; FAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 47 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; FEATURE:

; NAME/KEY: NRG3 EGF-like domain/amino acid seq.

; LOCATION: 1-47

; IDENTIFICATION METHOD:

; OTHER INFORMATION:

; US-09-126-121-4

; RESULT 3

US-09-126-121-8

; Sequence 8, Application US/09126121

; Patent No. 6352051

; GENERAL INFORMATION:

; APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao

; TITLE OF INVENTION: Erbb Receptor-Specific Neuregulin Related

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Winpatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/126,121

; FILING DATE: 30-Jul-1998

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Conley, Deidre L.

; REGISTRATION NUMBER: 36,487

; REFERENCE/DOCKET NUMBER: P1084R1D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/952-2066

; FAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 47 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

FEATURE: NAME/KEY: NRG3 EGF-like domain/amino acid seq.

LOCATION: 1-47 IDENTIFICATION METHOD: OTHER INFORMATION: US-09-126-121-8

Query Match Best Local Similarity 100.0%; Score 277; DB 4; Length 47; Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HFKPCRDKLAYCLNGECECFVETLGSHKHCRCKEGYQGVRCDFL 47

Db 1 HFKPCRDKLAYCLNGECECFVETLGSHKHCRCKEGYQGVRCDFL 47

RESULT 5 Sequence 7, Application US/08899437

PATENT NO. 6121415

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao

TITLE OF INVENTION: Erbb Receptor-Specific Neuregulin Related

TITLE OF INVENTION: Ligands and Uses Therefor

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

ZIP: 94080

GENERAL INFORMATION:

COMPUTER READABLE FORM: COMPUTER TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US09/126,121

FILING DATE: 30-Jul-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Conley, Deirdre L.

REGISTRATION NUMBER: 36,487

REFERENCE/DOCKET NUMBER: P1084R1D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/952-2066

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 360 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

FEATURE:

NAME/KEY: HNRG3 extracellular domain/Amino Acidseq

LOCATION: 1-360

IDENTIFICATION METHOD:

OTHER INFORMATION:

US-09-126-121-7

Query Match Best Local Similarity 100.0%; Score 277; DB 4; Length 360; Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HFKPCRDKLAYCLNGECECFVETLGSHKHCRCKEGYQGVRCDFL 47

Db 286 HFKPCRDKLAYCLNGECECFVETLGSHKHCRCKEGYQGVRCDFL 332

RESULT 7 Sequence 3, Application US/08899437

PATENT NO. 6121415

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao

TITLE OF INVENTION: Erbb Receptor-Specific Neuregulin Related

TITLE OF INVENTION: Ligands and Uses Therefor

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

ZIP: 94080

GENERAL INFORMATION:

COMPUTER READABLE FORM: COMPUTER TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08899437

FILING DATE: 24-Jul-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Conley, Deirdre L.  
 REGISTRATION NUMBER: 36,487  
 REFERENCE/DOCKET NUMBER: P1084R1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-2066  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 362 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear

FEATURE:  
 NAME/KEY: mNRG3 extracellular domain amino acid seq  
 LOCATION: 1-362  
 IDENTIFICATION METHOD: —  
 OTHER INFORMATION:  
 US-08-899-437-3

Query Match: 100 %; Score 277; DB 3; Length 362;  
 Best Local Similarity 100 %; Pred. No. 1e-25; 0; Mismatches 0; Indels 0; Gaps 0  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 HFKPCRDKDIALYCLNDGECVIETLGSNSHHRCKRCREGYQGVRCDFL 47  
 Db 288 HFKPCRDKDIALYCLNDGECVIETLGSNSHHRCKRCREGYQGVRCDFL 334

RESULT 9  
 US-08-899-437-23  
 ; Sequence 23 Application US/0899437  
 ; Patent No. 612415

GENERAL INFORMATION:  
 APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao  
 TITLE OF INVENTION: Erbb Receptor-Specific Neuregulin Related  
 TITLE OF INVENTION: Ligands and Uses Therefor  
 NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/899, 437  
 FILING DATE: 24-Jul-1997  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Conley, Deirdre L.  
 REGISTRATION NUMBER: 36,487  
 REFERENCE/DOCKET NUMBER: P1084R1

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-2066  
 TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 23:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 696 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear

FEATURE:  
 NAME/KEY: Human NRG3B2  
 LOCATION: 1-696  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION:  
 US-08-899-437-23

Query Match: 100 %; Score 277; DB 3; Length 696;  
 Best Local Similarity 100 %; Pred. No. 2e-25; 0; Mismatches 0; Indels 0; Gaps 0  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 HFKPCRDKDIALYCLNDGECVIETLGSNSHHRCKRCREGYQGVRCDFL 47  
 Db 286 HFKPCRDKDIALYCLNDGECVIETLGSNSHHRCKRCREGYQGVRCDFL 332

RESULT 10  
 US-09-126-121-23  
 ; Sequence 23 Application US/09126121  
 ; Patent No. 6252051

GENERAL INFORMATION:  
 APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao  
 TITLE OF INVENTION: Erbb Receptor-Specific Neuregulin Related  
 TITLE OF INVENTION: Ligands and Uses Therefor  
 NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WinPatIn (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/126,121  
 FILING DATE: 30-Jul-1998  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Conley, Deirdre L.  
 REGISTRATION NUMBER: 36,487  
 REFERENCE/DOCKET NUMBER: P1084R1D1  
 TELEPHONE: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 23:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 713 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 FEATURE:  
 NAME/KEY: Mouse NRG3 (mNRG3)/amino acid seq.  
 LOCATION: 1-713  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION:  
 US-08-899-437-2

Query Match 100.0%; Score 277; DB 4; Length 713;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-25;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HFPCRDKDLYCLNLDGECFVIELTGSHKICRKCKESYQGRCDQFL 47  
 288 HFPCRDKDLYCLNLDGECFVIELTGSHKICRKCKESYQGRCDQFL 334

RESULT 12  
 US/09/126,121-2  
 Sequence 2, Application US/09/126,121  
 Patent No. 6252031

GENERAL INFORMATION:  
 APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao  
 TITLE OF INVENTION: Erbb Receptor-Specific Neuregulin Related  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WinPatIn (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/126,121  
 FILING DATE: 30-Jul-1998  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Conley, Deirdre L.  
 REGISTRATION NUMBER: 36,487  
 REFERENCE/DOCKET NUMBER: P1084R1D1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 713 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 FEATURE:  
 NAME/KEY: Mouse NRG3 (mNRG3)/amino acid seq.  
 LOCATION: 1-713  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION:  
 US-09-126-121-2

Query Match 100.0%; Score 277; DB 4; Length 713;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-25;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HFPCRDKDLYCLNLDGECFVIELTGSHKICRKCKESYQGRCDQFL 47  
 288 HFPCRDKDLYCLNLDGECFVIELTGSHKICRKCKESYQGRCDQFL 334

RESULT 13  
 US-08-899-437-6  
 ; Sequence 6, Application US/08899437  
 ; Patent No. 6121415  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao  
 ; TITLE OF INVENTION: ErBB Receptor-Specific Neuregulin Related  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 ; OPERATING SYSTEM: IBM PC compatible  
 ; SOFTWARE: WinPatin (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/126,121  
 ; FILING DATE: 30-Jul-1998  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Conley, Deirdre L.  
 ; REGISTRATION NUMBER: 36,487  
 ; REFERENCE/DOCKET NUMBER: P1084R1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650/952-2066  
 ; TELEFAX: 650/952-9881  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 720 amino acids  
 ; TYPE: Amino Acid  
 ; TOPOLOGY: Linear  
 ; FEATURE:  
 ; NAME/KEY: hnRG3B1 amino acid sequence  
 ; LOCATION: 1-720  
 ; IDENTIFICATION METHOD:  
 ; OTHER INFORMATION:  
 ; US-08-899-437-6

Query Match 100.0% Score 277; DB 3; Length 720;  
 Best Local Similarity 100.0% Pred. No. 2.1e-25; Matches 47; Conservatve 0; Mismatches 0; Indels 0; Gaps 0; Db 286 HFKPCRDKDLYCLNDGECFVIETLGSHKHCRCKEGYOGVRQDQFL 332

RESULT 14  
 US-09-126-121-6  
 ; Sequence 6, Application US/09126121  
 ; Patent No. 625051  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao  
 ; TITLE OF INVENTION: ErBB Receptor-Specific Neuregulin Related  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: IBM PC compatible  
 ; SOFTWARE: WinPatin (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/417,640A  
 ; FILING DATE: 24-Jul-1997  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Conley, Deirdre L.  
 ; REGISTRATION NUMBER: 36,487  
 ; REFERENCE/DOCKET NUMBER: P1084R1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650/952-2066  
 ; TELEFAX: 650/952-9881  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 720 amino acids  
 ; TYPE: Amino Acid  
 ; TOPOLOGY: Linear  
 ; FEATURE:  
 ; NAME/KEY: hnRG3B1 amino acid sequence  
 ; LOCATION: 1-720  
 ; IDENTIFICATION METHOD:  
 ; OTHER INFORMATION:  
 ; US-09-126-121-6

Query Match 100.0% Score 277; DB 4; Length 720;  
 Best Local Similarity 100.0% Pred. No. 2.1e-25; Matches 47; Conservatve 0; Mismatches 0; Indels 0; Gaps 0; Db 286 HFKPCRDKDLYCLNDGECFVIETLGSHKHCRCKEGYOGVRQDQFL 332

RESULT 15  
 US-08-417-640A-1  
 ; Sequence 1, Application US/08417640A  
 ; PATENT NO. 5670342  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carnahan, Jostette F.  
 ; APPLICANT: Harra, Shinichi  
 ; APPLICANT: Lu, Hsieng S.  
 ; APPLICANT: Mayer, John P.  
 ; APPLICANT: Yoshihaga, Steven K.  
 ; TITLE OF INVENTION: NDP Peptides  
 ; NUMBER OF SEQUENCES: 6  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Amgen Inc.  
 ; STREET: 1840 De havilland Drive  
 ; CITY: Thousand Oaks  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 91320  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: IBM PC compatible  
 ; SOFTWARE: WinPatin (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/417,640A  
 ; FILING DATE: 24-Jul-1997  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mazza, Richard J.  
 ; REFERENCE/DOCKET NUMBER: A-310  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 52 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein

US-08-417-640A-1

Search completed: November 7, 2002, 10:03:19  
Job time : 14 secs